25th Conference of the Austrian Society of Plant Biology

29th to 31st of May 2025, Tulln an der Donau

Book of Abstracts

Organizing committee

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Program overview

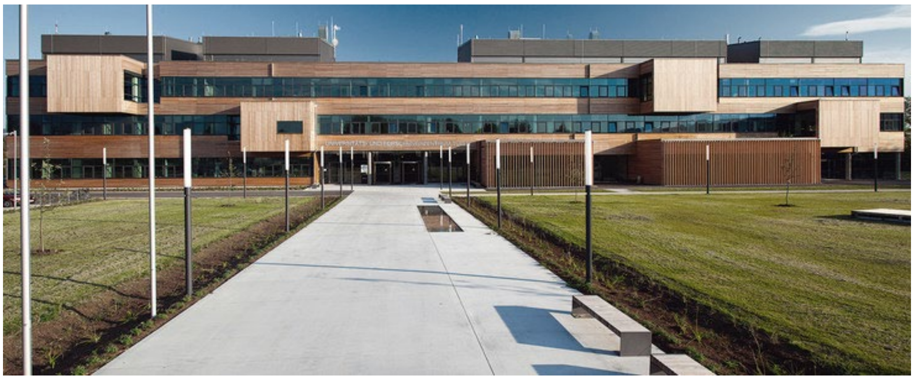
	Thursday 29.05.2025	Friday 30.05.2025	Saturday 31.05.2025
08:40		**Session 3** *Ecophysiology and Environmental Stress in Trees*	**Session 7** *Plant Morphology, Phenology and Function*
09:00			
09:20			
09:40			
10:00			
10:20		**Coffee Break**	**Coffee Break**
10:40		**Session 4** *Multi-Omics Perspectives in plant science*	**Session 8** *Environmental Factors and Plant Biochemistry*
11:00			
11:20			
11:40	Registration		
12:00			
12:20		**Lunch break**	**Closing ceremony**
12:40			
13:00	**Opening**		
13:20	**Session 1** *Arabidopsis as a Model: Molecular Insights into Stress Responses*	**Free poster viewing** **Short excursions:** *1 0000 years of cereal history* *Phenotyping of grapevine*	Post-conference activities
13:40			
14:00			
14:20			
14:40		Session 5 *Responses of Crops to Changing Environments*	
15:00			
15:20	**Coffee Break**		
15:40	**Session 2** *Crop Physiology and Stress Adaptation*		
16:00		**Coffee Break**	
16:20		**Session 6** *Molecular Insights into Plant Growth and Stress Response*	
16:40			
17:00			
17:20	**Poster session**		
17:40			
18:00	**Ice breaker**	**Poster session**	
18:20			
18:40		**Poster session/ATSPB Meeting**	
19:00		**ATSPB meeting**	
19:20			
19:40		**Conference dinner**	
20:00			
20:20			
20:40			
21:00			

Location

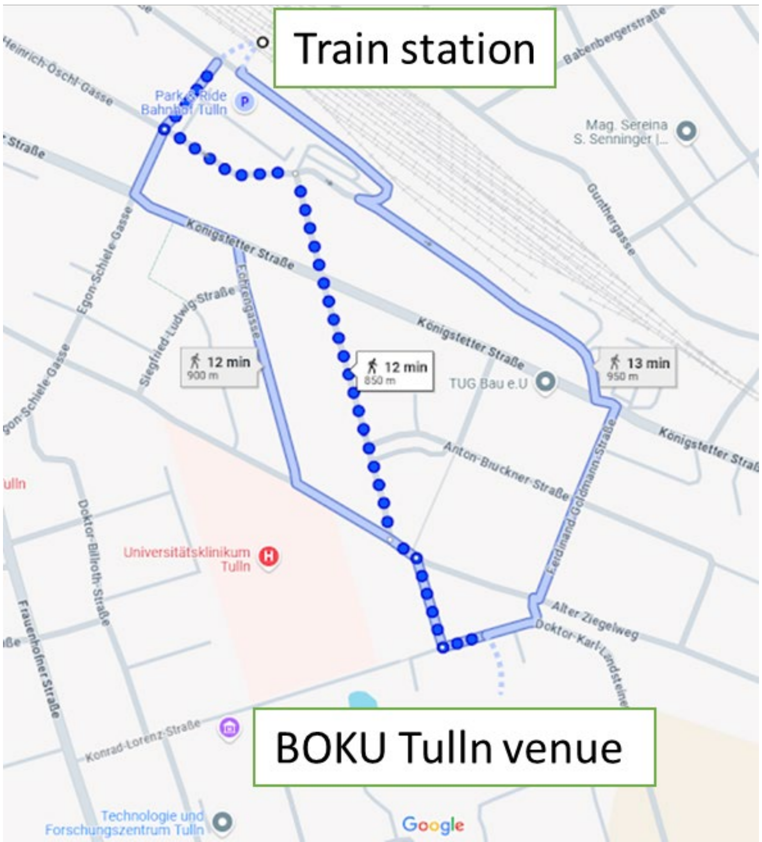
University and Research Center Tulln (UFT, Konrad-Lorenz-Str. 24, 3430 Tulln an der Donau)

Assembly hall (https://navi.boku.ac.at/?q=UFT,%20Hauptgeb%C3%A4ude)

Main entrance:



Map from the train station to conference venue:



Oral Presentations

Please hand in your presentation as a PDF/PPTX via USB stick during registration.

Session 1: Arabidopsis as a Model: Molecular Insights into Stress Responses

Thursday, 29.05.2025

1A	13:20	Norouzi, Hooman	Temperature-dependent modulation of DNA repair pathways during seed development in *Arabidopsis thaliana*
1B	13:40	Bonn, Christina	Chilling night events lead to different adaptations of the central carbohydrate metabolism than acclimation to permanent cold
1C	14:00	Fürtauer, Lisa	Cytosolic fructose - an underestimated player in the regulation of sucrose biosynthesis
1D	14:20	Zhang, Xingjian	The role of sucrose transporter regulation in the *Arabidopsis* salt stress response
1E	14:40	Anwar, Maaz	Functional characterization of BBE proteins in *Arabidopsis*
1F	15:00	Falter, Pia Marina	Invertases shape the nocturnal heat response and acclimation in Arabidopsis thaliana ecotype-specifically

Session 2: Crop Physiology and Stress Adaptation

2A	15:40	Farolfi, Elena	The role of time, temperature, and drought on the osmotic adjustment of grapevines
2B	16:00	Mosleh, Iman Samiei	A Multi-Omics Exploration of Magnesium Deficiency in Welschriesling Grapevines
2C	16:20	Mandl, Karin	Vines take up yeasts from soil and transport them through the vine to the stem and skins of grapes
2D	16:40	Osterkamp, Susanne	Impact of Supplemental Light Spectra on Morphological and Phytochemical Traits of *Brassica oleracea* Microgreens
2E	17:00	Chen, Tsu-Wei	High-Throughput Phenotyping of Stomatal Traits: Novel Selection Targets to Design Stress Tolerance in Wheat

Session 3: Ecophysiology and Environmental Stress in Trees

Friday, 30.05.2025

3A	8:40	Hesse, Benjamin D.	Do calculations based on visually assessed sapwood depth underestimate the water use of oak trees?
3B	9:00	Fitzky, Anne Charlott	Ozone uptake and Ozone-Induced Oxidative Stress: A Comparative Study of Urban Tree Species on a hot summer day

3C	9:20	Ahmad, Muhammad	Natural variation in drought sensitivity and associated metabolome under soil drying in European black pine (*Pinus nigra* Arnold s.l.)
3D	9:40	López-Hidalgo, Christina	The Road Taken Makes All the Difference: Order-Dependent Molecular Acclimation of *Pinus pinaster* to Heat and Drought Stress
3E	10:00	Onoszko, Katherine	Physiological responses of holm oak (*Quercus ilex* L.) seedlings to biotic stress and eco-friendly mitigation strategies for forest decline
Session 4: Multi-Omics Perspectives in plant science			
4A	10:40	Weckwerth, Wolfram	PANOMICS – a paradigm shift in plant biology
4B	11:00	Jonak, Claudia	Diverse adaptive responses to heat and drought in the climate-resilient crop *Camelina sativa*
4C	11:20	Montrucchio, Elisa	Cellular Redox Status and Carbohydrate Metabolism in the Old Oilseed Crop Camelina under Drought and Waterlogging Stress
4D	11:40	Stegner, Moritz	Exploring drought-induced metabolic changes in montane conifers
4E	12:00	Chaturvedi, Palak	Crops in a changing climate environment – a MULTIOMICS perspective
Session 5: Responses of Crops to Changing Environments			
5A	14:40	Fekonja, Susanne Katharina	Biochemical Adaptations of Tomato Plants (*Solanum lycopersicum* L.) in Response to Environmental Stress and Biotic Interactions
5B	15:00	Ijaz, Bushra	Investigating the Role of Calcium-Dependent Protein Kinases in Potato Tuber Formation
5C	15:20	Prasad, Manoj	Role of HDA9-HDA19-HAT3 repressor complex during dehydration stress in C4 model crop foxtail millet [*Setaria italica* L.]
5D	15:40	Balas, Johannes	Investigating the unique attributes of the European bilberry on natural stands: implications for cultivation and regional value creation
Session 6: Molecular Insights into Plant Growth and Stress Response			
6A	16:20	Apon, Fariha	Early response to nickel on root growth, cell wall alteration and THESEUS1 dependent phosphoregulation
6B	16:40	Retzer, Katarzyna	KIN10 is Required to Orchestrate Efficient Cell Elongation in Response to Pathogen Attack and Light

6C	17:00	Bachmair, Andreas	Plant resilience at the molecular level: How protein modification helps to withstand stressful conditions
6D	17:20	Wurzinger, Bernhard	proximity labelling enters plastids
6E	17:40	Harencar, Lubomir	An integrated database of antiglycan monoclonal antibodies based on a complex meta-analysis of published data
Session 7: Environmental Factors and Plant Biochemistry Saturday, 31.05.2025			
7A	8:40	Górska, Alicja	Exploring the role of HIPP proteins in regulating auxin responses
7B	9:00	Ufimov, Roman	Complex Speciation in Crataegus: Unraveling Hybridization, Polyploidy, and Apomixis in Central Europe
7C	9:20	Tiloca, Guiseppe	Phenotypic and Chemical Cuticle Plasticity in *Kalmia procumbens*
7D	9:40	Bartrina, Isabel	Root-derived cytokinin regulates flowering time in Arabidopsis thaliana
7E	10:00	Schillaci, Luigi	Exploring heavy metal localization in mosses using nanoscale x-ray imaging
Session 8: Plant Morphology, Phenology and Function			
8A	10:40	Antreich, Sebastian J.	Fatigue cracks in trees and walnuts
8B	11:00	Stumpe, Eric	3D Multimodal Image Registration for Plant Phenotyping
8C	11:20	Niedermeier, Martin	Multi-scale Characterization of Cotton Fiber Structure and Properties
8D	11:40	Liesche, Johannes	How conifers and grasses overcome physical limits to sugar export from leaves
8E	12:00	Kranner, Ilse	Seed sorting via infrared thermography reveals hidden metabolic signatures of ageing

Poster Presentations

Please hang your poster to the assigned poster wall.

P1	Asayesh, Zeinab Maleki	Adaxial additional Stomata in *Phylloxera*-Infested Leaves: Benefit and role?
P2	Ashraf, Suhail	Deciphering Genetic Determinants of Delayed Ripening in Grapevine through RNA-Seq Analysis
P3	Auricht, Hannah-Sophie	Using gas chromatography and mass spectrometry (GC-MS) for the detection of drought stress effects on the metabolome of Solanum tuberosum varieties
P4	Auricht, Hannah-Sophie	Metabolic changes of *Paraburkholderia dioscoreae* strain Msb3 on varying substrates
P5	Balas, Johannes	The Slow-flower movement. Contribution to sustainability in floriculture
P6	Balekoglu, Safa	*Pinus pinea* seedlings demonstrated high resilience in a short but severe drought, indicated by their adaptive biochemical responses
P7	Bellaire, Anke	Ultrastructural analysis of *Clusia* chloroplasts with varying CAM physiotypes
P8	Boszorádová, Eva	Identification of a peculiar chitinase in carnivorous plant species *Drosera binata*
P9	Wernig, Stefanie	The influence of drought stress on mosses and liverworts
P10	Charalambou, Paraskevi	Cuticle of Kalmia procumbens leaves: flavonoids form spines for defence?
P11	Danchenko, Monika	Identification and molecular cloning of a unique protease from carnivorous sundew
P12	Djohan, Yovita Astuti	Increased pathogen resilience in Pea: Deciphering the Metabolic Code
P13	Fateminia, Seyedehfaezeh	In vitro Propagation of Ferns
P14	Fink, Marion	Crown transparency influences growth dynamics in *Pinus sylvestris* and *Juniperus communis*
P15	Fitzky, Anne Charlott	The role of the green cortex in stems from Winter to Spring in *Carpinus betulus* under salt stress
P16	Fladenhofer, Lea	Does H_2S positively influence sulfur metabolism in C4 plants?
P17	Gavurová, Martina	Scytonemin from Nostoc commune: A natural compound inducing apoptosis in leukemia cells
P18	Goga, Michal	Allelopathic effect of lichen secondary metabolites on a photobiont *Asterochloris erici*
P19	Heinzel, Paula	The lichenization of *Cladonia grayi*: from free-living symbionts to thallus formation
P20	Heschl, Sandro M.	Underneath agrivoltaics Physiological study on cherries
P21	Hesse, Benjamin D.	A Low-Cost Automated Irrigation System Using Mini-Lysimeters for Improved Drought Stress Experiments with Juvenile Trees
P22	Hittorf, Michaela	Phytomyxids and their interactions with their hosts
P23	Teige, Markus	Potato stress acclimation and signaling under abiotic stress

P24	Innocenti, Jacopo	A single-berry level study on the effect of moderate to severe heat waves on berry cell death in grapevine
P25	Just, Josefine	Impacts of Heavy Metals and Substrate-pH on the Growth of two Moss Species
P26	Khalil, Sarhan	Iron homeostasis in grapevine rootstocks: Understanding the adaptive mechanisms in response to low iron availability conditions
P27	Knaipp, Elisabeth	Chlorophyll a fluorescence as a reliable parameter for photosynthetic activity
P28	Koch, Hanna	Exploring the role of endophytes for improving cryopreservation of potato
P29	Kovacs, Dorottya; Michels, Gustav K.	Towards a new categorization of the anatomical structure of lenticels
P30	Kryvokhyzha, Maryna	Proteomic analysis of germinating seeds of parasitic weed—branched broomrape (*Phelipanche ramosa*)
P31	Li, Mengke	Soil microbiome dynamics in response to root exudates from wheat and pearl millet
P32	Linhart, Lea	Water relations of Grüner Veltliner vines unaffected by rootstock variability
P33	Luskova, Tereza	Understanding Concept Drift in Metabolomics: Predictive analysis of *Arabidopsis thaliana* under cold stress conditions
P34	Merkel, Patrizia	Exploring seasonal variations in pigment and antioxidant contents, and the effects of recurrent droughts in *Picea abies* and *Larix decidua*
P35	Mosleh, Iman Samiei	Magnesium Deficiency Disrupts Photosynthetic Performance in Welschriesling: Evidence from Dynamic Gas Exchange Modeling
P36	Mosleh, Iman Samiei	Integrative Transcriptomic and Network Analysis Revealed Candidate Genes Underlying Dwarfism in Rye (*Secale cereale* L.)
P37	Münchinger, Ines K.	Quantifying Gas Exchange Through Periderm and Lenticels: A Multi-Method Analysis in Branches of Varying Ages of Central European Tree Species
P38	Onoszko, Katherine	Diversity patterns of herbaceous community in environmental gradients of dehesa ecosystems
P39	Peters, Feline	Inter- and Intraspecific Variation in Elemental Concentrations in Alpine Plants
P40	Posada, Jorge	The best way to stain with Calcofluor White, an example in moss cells.
P41	Rashkov, Georgi	Influence of Anthocyanins on the Photosynthetic Response of Two Basil Varieties Under Drought Stress
P42	Retzer, Katarzyna	Dynamic Dark Root Chamber (DDrC): A Novel Approach for Non-Invasive Root Phenotyping in Darkness
P43	Routray, Deepti	Proteomic Insights into the Allelopathic Effects of Usnic Acid on Physcomitrium patens
P44	Santangeli, Michael	Thirsty roots: How short-term drought shapes maize (*Zea mays* L.) root exudation patterns

P45	Schinnerl, Viktoria	Seasonal variations in metabolite and transcript profiles in the streptophyte green alga *Zygogonium ericetorum*
P46	Spiridon, Andreea	Root trait adaptation under drought for resilient cropping systems: Insights from two faba bean genotypes grown in different soils
P47	Stefanov, Martin	Effect of humic acid on photosynthetic activity of green basil under drought stress
P48	Tenhaken, Raimund	Galactose toxicity in plants – a paradox
P49	Vörös, Weronika A.	Unraveling Local Decline in *Antennaria dioica* Populations through time: The Role of Genetic Diversity, Sex Ratios, and Environmental Factors
P50	Weinberger, Matthias	Synchrotron source X-ray experiments reveal element specific distributions of heavy metals in moss leaves

Oral presentations – Overview

Thursday, May 29, 2025

Session 1: Arabidopsis as a Model: Molecular Insights into Stress Responses

Session chair: Thomas Werner

Session 2: Crop Physiology and Stress Adaptation

Session chair: Jose-Carlos Herrera

Friday, May 30, 2025

Session 3: Ecophysiology and Environmental Stress in Trees

Session chair: Andreas Holzinger

Session 4: Multi-Omics Perspectives in plant science

Session chair: Fatemeh Maghuly

Session 5: Responses of Crops to Changing Environments

Session chair: Raimund Tenhaken

Session 6: Molecular Insights into Plant Growth and Stress Response

Session chair: Wolfram Weckwerth

Saturday, May 31, 2025

Session 7: Environmental Factors and Plant Biochemistry

Session chair: Ilsa Kranner

Session 8: Plant Morphology, Phenology and Function

Session chair: Ingeborg Lang

1A: Temperature-dependent modulation of DNA repair pathways during seed development in *Arabidopsis thaliana*

Hooman Norouzi[1*], Erwann Arc[1], Sajjad Awan[2], Wim Soppe[3,4], Natanael Viñegra[3], Thomas Roach[1], Loic Rajjou[5], William Finch-Savage[2], Ilse Kranner[1]

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(4) Rijk Zwaan Breeding B.V., Burgemeester Crezéelaan 40 2678 ZG De Lier, The Netherlands
(5) Jean-Pierre Bourgin Institute, INRAE, AgroParisTech, Université Paris-Saclay, Versailles, France

** Presenting author: Hooman.Norouzi@uibk.ac.at*

High-quality seeds are key to agricultural productivity and conservation, yet the mechanisms of how environmental factors during seed development shape seed quality traits, such as vigour, are not fully understood. *Arabidopsis thaliana* plants were exposed to control (CT: 18_{night}-22_{day}°C), lowered (LT: 14_{night}-16_{day}°C), and elevated temperatures (ET: 25_{night}-28_{day}°C), under a 16-8 h light-dark cycle during seed development after growth under CT until flowering. Mature dry seeds were studied using RNASeq. ET led to lower yield but larger seeds, whereas LT seeds were smaller and least vigorous. Gene products involved in several DNA repair pathways showed differential accumulation depending upon maternal temperature regimes, with many up-regulated under LT. These included *RAD54* and *MRE11*, involved in homologous recombination, *LIG4*, a seed longevity determinant involved in non-homologous end joining, and genes associated with base excision repair, including *ARP* and *DML1/2*, or nucleotide excision repair, such as *CSA1/2* and *RAD23A*. The results suggest that the temperatures experienced during seed development modulate key DNA repair pathways in mature dry seeds. However, the impact of the maternal environment on genome integrity remains to be elucidated.

1B: Chilling night events lead to different adaptations of the central carbohydrate metabolism than acclimation to permanent cold

Christina Bonn[1*], Oliver Giesbrecht[1], Mona Becker[1], Sofie Jennings[1], Anna Matuszyńska[2], Lisa Fürtauer[1]

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Plants often experience significant temperature fluctuations due to chilling night events in spring and autumn. Yet, the impact of chilling nights followed by warm days is seldom addressed as typical cold acclimation studies involve constant cold conditions during both day and night. Therefore, we investigated within the central carbohydrate metabolism how *Arabidopsis th.* responds to nights at 4 °C followed by days at 22 °C through a time-series analysis. Carbohydrate concentrations and maximum enzyme activities were determined. After the first night, content of carbohydrates like sucrose, glucose and fructose was increased for the first hours of the day; however, at the end of the day levels were similar to those of control plants except for glucose, which remained significantly elevated. While no changes in maximum enzyme activity were observed after the initial chilling night, after six chilling nights, the maximum sucrose phosphate synthase (SPS) activity increased two-fold, whereas sucrose levels elevated three-fold and starch levels remained unchanged. This contrasts with findings from cold acclimation studies that report no significant increase in v_{max} of SPS and a 4-10-fold increase in starch concentration[1,2]. Even though the SPS v_{max} was increased sucrose concentrations were only elevated to the same extend as in permanent cold[1,2]. We conclude, also supported by mathematical modelling approaches, that adaptation occurs shortly after the first chilling night and that long-term responses differ markedly from typical cold acclimation studies. Investigating the long-term effects of chilling nights may reveal a distinct regulatory strategy compared to conventional cold acclimation research.

References

[1] Kitashova, Anastasia; Schneider, Katja; Fürtauer, Lisa; Schröder, Laura; Scheibenbogen, Tim; Fürtauer, Siegfried; Nägele, Thomas. 2021. Impaired chloroplast positioning affects photosynthetic capacity and regulation of the central carbohydrate metabolism during cold acclimation. Photosynthesis Research, 1: 49-60.

[2] Kitashova, Anastasia; Adler, Stephan O.; Richter, Andreas S.; Eberlein, Svenja; Dziubek, Dejan; Klipp, Edda and Nägele, Thomas. 2023. Limitation of sucrose biosynthesis shapes carbon partitioning during plant cold acclimation. Plant, Cell & Environment, 2: 464-478.

1C: Cytosolic fructose - an underestimated player in the regulation of sucrose biosynthesis

Oliver Giesbrecht[1], Christina Bonn, Lisa Fürtauer[1]*

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** Presenting author: Lisa.Fuertauer@bio3.rwth-aachen.de*

Plants must continuously adapt to environmental fluctuations, significantly influencing their photosynthetic performance and overall metabolism. The sucrose cycling system, with a continuous synthesis and degradation of sucrose, plays a critical regulatory role during stress conditions. We were interested in the regulatory strategies of this crucial cycling system, and investigated mathematically system stabilities [1]. Specifically, we determined the effects of mutations within this cycle by HEXOKINASE1 (*Arabidopsis thaliana*, *gin2-1*), alongside high-light exposure. Incorporating experimental subcellular metabolite data into a Structural Kinetic Model (SKM) allowed exploration of regulatory responses within a three-compartment model. Our models under high-light stress demonstrated increased system stabilities for the tested regulations, with *gin2-1* being more sensitive than its wildtype. Additionally, we confirmed that phosphorylated sugars serve as stronger activators of sucrose-phosphate synthase (SPS) than glucose does. Interestingly, models with fructose SPS activation exhibited similar stability patterns. Consequently, we proposed and verified *in silico* a triple activation of SPS by highly activating phosphorylated sugars and lower activating non-phosphorylated hexoses. Subsequently, we biochemically confirmed the previously unknown activation of SPS by fructose *in vitro*. In summary, our study highlights the essential role of sucrose cycling in plant cells under stress conditions and reveals that phosphorylated sugars are stronger activators of SPS than glucose while introducing a novel activation mechanism by cytosolic fructose. These findings underscore the efficiency of our systems biology approach and provide valuable insights into carbohydrate metabolism regulation, paving the way for future investigations into sucrose cycling complexities in plants.

References

[1] Giesbrecht Oliver, Bonn Christina, Fürtauer Lisa. (2024). Cytosolic fructose - an underestimated player in the regulation of the sucrose biosynthesis? bioRxiv: 2024.2012.2011.628007.

1D: The role of sucrose transporter regulation in the Arabidopsis salt stress response

Xingjian Zhang[1*], Johannes Liesche[1]

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Photosynthetically produced carbohydrates are transported from green leaves to carbon sink tissues like roots and seeds to support plant growth and development. Regulating this transport is crucial for balancing whole-plant carbon allocation under varying environmental conditions. A key step is the loading of sucrose into the phloem in leaf veins. In *Arabidopsis thaliana*, this step is facilitated by the companion cell-specific sucrose transporter SUC2. We could previously demonstrate that post-translational regulation of SUC2 is decisive for setting leaf carbon export rates. Here, we present two kinases, WAKL8 and PBL5, as potential regulators of SUC2. Their roles were investigated using genetic and biochemical approaches. WAKL8 is associated with light-dependent regulation, while PBL5 is linked to the salt stress response. *In vitro* and *in vivo* assays confirmed that both kinases phosphorylate SUC2. Functional analysis in *Nicotiana benthamiana* showed that phosphorylation-site mutations in SUC2 reduced sucrose transport efficiency. In *Arabidopsis*, loss-of-function mutants of *wakl8* and *pbl5* exhibited increased SUC2 activity and enhanced phloem loading. These mutants also displayed improved growth under salt stress, suggesting that phosphorylation negatively regulates SUC2 activity to fine-tune sucrose transport under stress. Our results demonstrate that phosphorylation modulates SUC2 function and contributes to salt stress adaptation, highlighting a post-transcriptional mechanism with potential relevance for improving crop resilience.

1E: Functional characterization of BBE proteins in *Arabidopsis*

Maaz Anwar[1*], Tomas Werner[1]

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Berberine bridge enzyme (BBE)-like proteins belong to the FAD-linked oxidoreductase superfamily and play a role in alkaloid biosynthesis in many plants. Although *Arabidopsis thaliana* lacks complex alkaloids, its genome encodes 27 BBE-like protein, suggesting additional functions. These proteins are classified into seven clusters, with biochemical evidence indicating that some members oxidize monolignols, the building blocks of lignin. Our research focuses on phylogenetically closely related *BBEs* – namely *BBE13, -15, -24, -25, and -26* – and their potential role in lignin biosynthesis regulation. To functionally characterize these proteins in *Arabidopsis*, we generated single and higher order loss-of-function mutants, along with *BBE* overexpression lines. Phenotypic analyses of these mutants revealed morphological changes in lignified structures of roots and stems, emphasizing the role of BBEs in lignification. To investigate *BBE* expression patterns, we generated transcriptional reporter lines, which showed distinct expression profiles in lignified tissues. Additionally, to determine the subcellular localization of BBEs, we expressed fluorescent protein-tagged BBEs in *Nicotiana benthamiana* leaves. Confocal laser scanning microscopy revealed BBEs localization in the apoplast, which is consistent with the proposed subcellular compartmentation of the lignin biosynthesis machinery. This further supports the potential role of BBEs in regulating cell wall components. Overall, our research explores the role of BBEs in regulating lignin content and composition, highlighting their involvement in lignification as well as pointing to additional functions in plant development.

1F: Invertases shape the nocturnal heat response and acclimation in *Arabidopsis thaliana* ecotype-specifically

Pia Marina Falter[1*,#], Christina Bonn[1,#], Lisa Fürtauer[1]

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 # contributed equally

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Due to climate change, temperature extremes and amplitude variations increase, which poses major challenges on the short term response and acclimation capacities of plants to abiotic stresses [1]. In the scope of temperature acclimation research, temporal resolution tended to miss the dynamics of diurnal responses and acclimation. Therefore, we resolved dynamically over time how *Arabidopsis* ecotypes react to heat exposure. Plants of the ecotype Col-0, the heat-tolerant accession C24 and heat-sensitive Rsch were treated with elevated temperatures for 1, and 3 days. The impact of diurnal heat at 32 °C (ΔT = 12 °C) and a nocturnal elevation to 20 °C (ΔT = 2 °C) compared to controls (12h/12h at 22 °C/ 18 °C) was analyzed regarding components of the primary carbohydrate metabolism focusing on nocturnal alterations. The results indicated ecotype-specific acclimation strategies: while the ecotypes shared general tendencies such as starch depletion, they diverge in the redistribution of soluble sugars. During heat acclimation Rsch accumulated sucrose, while C24 adjusted hexose accumulation throughout the night. Subsequently, invertase maximum activities revealed different stress and acclimation responses, corresponding in the dynamics to the ecotype-specific temperature optimum of the respective climate adaptation. Within three days, the ecotypes adapted their sugar metabolism mostly by upregulating invertase activities and re-adjusting or enhancing soluble sugar concentrations. In conclusion, the ecotypes followed distinct strategies in response to heat, with invertase activities being a putative main driver of the nocturnal soluble carbohydrate re-distribution strategies.

References

[1] Seth P., Sebastian J. 2024. Plants and global warming: challenges and strategies for a warming world. Plant Cell Rep., 42:27.

2A: The role of time, temperature, and drought on the osmotic adjustment of grapevines

Elena Farolfi[1*], Adéla Kulhánková[2,] Federica De Berardinis[1], Soma László Tarnay[1], Gregory A. Gambetta[3], Uri Hochberg[4], Astrid Forneck[1], Jose Carlos Herrera[1]

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Osmotic adjustment (OA) is a crucial physiological mechanism that enables plants to tolerate drought by accumulating osmolytes. However, the seasonal dynamics of OA and its interaction with temperature and water availability remain poorly understood. We investigated the effects of temperature and water availability under controlled greenhouse conditions. Plants were grown at three different temperature regimes (20°C, 25°C, and 30°C). Within each temperature, two water treatments (well-watered and water deficit) were imposed for 35 days. Leaf osmotic potential at full turgor (π_{100}) was measured using an osmometer, while sugar and cation concentrations were analysed through high-performance ion chromatography. π_{100} decreased progressively over time, indicating seasonal osmolyte accumulation. However, neither temperature nor water deficit significantly altered the rate of seasonal OA, although both factors influenced absolute π_{100}values. Sugars and cations accounted for 54.5% of the osmotic potential, with no single osmolyte dominating the OA response. The results indicate that a seasonal OA occurs consistently in grapevine and that such OA is not triggered as a response to changes in temperature or water status. The water deficit treatment was probably too mild (ca. -1MPa) to induce a stronger OA. Our findings indicate that grapevines exhibit a pre-programmed seasonal OA pattern independent from environmental variability. This osmoregulation strategy aligns with other Mediterranean and temperate-climate plants and provides insights for enhancing drought resilience under future climate scenarios.

Acknowledgements

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2B: A Multi-Omics Exploration of Magnesium Deficiency in Welschriesling Grapevines

Iman Samiei Mosleh[1*], Ferdinand Regner [2], Tamas Deak [3], Fatemeh Maghuly[1]

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Magnesium (Mg) deficiency is a critical limiting factor in viticulture, notably impacting the productivity and quality of Welschriesling (WR), a prominent grape variety in Austria and Central European vineyards. The prevalence of this deficiency is exacerbated in regions with light soils and high precipitation, leading to Mg leaching and subsequent physiological impairments. The inherent low Mg uptake efficiency of current WR clones necessitates the identification and development of genotypes with improved Mg acquisition and utilization. This research aims to elucidate the genetic and epigenetic determinants of enhanced Mg uptake in WR, employing an integrative multi-omics strategy. We conducted a comparative analysis of Mg-efficient (Mg+) and Mg-deficient (Mg-) clones of WR, integrating genomic, epigenomic, and transcriptomic datasets. PacBio long-read sequencing facilitated the identification of small variants using *DeepVariant* and structural variants with *DeBreak*. DNA methylation profiling was performed using the *IPDsummary* tool. Illumina short-read sequencing was used for gene expression analysis, and Mg-related candidate genes were identified through weighted gene co-expression network analysis (*WGCNA*). Our findings revealed significant variations in DNA methylation patterns, correlating with Mg uptake efficiency. This highlights the critical region for Magnesium uptake in *Vitis vinifera*. These results provide a foundation for the development of molecular markers to distinguish Mg-efficient WR clones, enabling targeted breeding and vineyard management strategies. Furthermore, this research offers insights applicable to other viticultural regions facing similar challenges, contributing to the sustainability and resilience of global grape production.

2C: Vines take up yeasts from soil and transport them through the vine to the stem and skins of grapes

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In a vineyard field experiment it was demonstrated that Saccharomyces cerevisiae yeast can be adsorbed from the soil by the rootsof *Vitis vinifera subs. vinifera* and transported via vine to the stems and surface of the grapes. To exclude any extrinsic yeast contamination, the ripening grapes were sterilized and wrapped in plastic bags. Eleven active dried yeasts from different companies were then spread onto the vineyard soil. At four different time points, grape samples were taken under sterile conditions, crushed, and fermented without further inoculation. The yeasts in the fermented musts were characterized by PCR fingerprinting using the ITS region, testing whether they belonged to the Saccharomyces species. Then a microsatellite PCR was carried out with S.cerevisiae to demonstrate that these yeasts in the fermented must were from the same yeasts spread on the vineyard soil. The results showed that four of the eleven yeasts spread in the vineyard were transported via the vines onto the skin of the grapes

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2D: Impact of Supplemental Light Spectra on Morphological and Phytochemical Traits of *Brassica oleracea* Microgreens

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Diet-related chronic diseases are rising across Europe, partly due to declining crop quality and unhealthy dietary habits. Microgreens—young, nutrient-dense plants—offer a sustainable and health-promoting food source, especially when cultivated in controlled environments. Light quality plays a key role in influencing microgreen growth and nutritional value, with species- and spectrum-specific responses. This study examined the effects of additional monochromatic light (blue, hyper red, green, and amber LEDs) combined with commercially used standard white fluorescent lighting on two *Brassica oleracea* microgreen cultivars: var. *palmifolia* and var. *sabellica*. The effects of the applied type of light were evaluated based on changes in plant morphology and secondary metabolites measured spectrophotometrically, including total phenolic content, flavonoids, anthocyanins, antioxidant capacity, chlorophylls and carotenoids. Supplemental green light significantly enhanced plant height, fresh mass, chlorophyll content, flavonoid levels, and antioxidant capacity in both varieties, while red light consistently resulted in the lowest values across most parameters. These findings underline the importance of customized light strategies in microgreen production and highlight green light's potential to enhance both yield and nutritional quality in controlled environment agriculture.

2E: High-Throughput Phenotyping of Stomatal Traits: Novel Selection Targets to Design Stress Tolerance in Wheat

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Stomatal morphology and its developmental plasticity affect water use efficiency and gas exchange and are critical for stress tolerance of crops under climate change. However, understanding the diversity of stomatal traits (STs) and their role in plant breeding remains limited, primarily due to challenges in phenotyping. Here, we present a high-throughput method for phenotyping stomatal morphology in wheat, paired with an automated computational pipeline that quantifies 24 stomatal traits related to size, variation, maximum stomatal conductance, and spatial distribution. Using this approach, we: (1) analyzed over 30,000 images from 60 wheat cultivars grown in growth chamber, greenhouse, and field conditions; (2) investigated the impact of light, temperature, drought, and nitrogen on STs and their developmental plasticity across adaxial and abaxial surfaces; and (3) evaluated the breeding progress of STs. Many STs exhibited high heritability within environments, with broad-sense heritability exceeding 67%, suggesting significant genetic regulation. Notably, STs were more heritable in field conditions than in growth chamber or greenhouse environments, with high correlation (R = up to 0.58) with growth chamber results from conditions most similar to the field. Environmental variability of STs (56-285%) provided insights into developmental plasticity in STs. Interestingly, stomatal length on the abaxial side correlated positively with leaf water content (R = 0.78), while shoot water content was more strongly associated with spatial divergence of stomata (R = 0.80). Breeding progress analyses indicated that genetic diversity of stomatal traits has been maintained, highlighting the potential of beneficial STs as new selection targets for enhancing stress tolerance and water use efficiency in high-yielding wheat cultivars.

3A: Do calculations based on visually assessed sapwood depth underestimate the water use of oak trees?

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Understanding how climate change affects tree- and stand-level water balance is essential for developing effective silvicultural strategies to mitigate its adverse impacts and ensure forest sustainability. Various methods exist for measuring xylem sap flow density (SFD), with each technique exhibiting distinct advantages and limitations. However, accurately estimating a tree's total water consumption requires not only well-calibrated SFD but also two additional parameters: the depth of conducting sapwood and the xylem sap flow profile, which describes the decrease in SFD from the outer to the inner sapwood. For ring-porous species, such as sessile oak (*Quercus petraea* (Mattuschka) Liebl.), conducting sapwood depth is traditionally assessed using the light transmission method combined with heartwood coloration, coupled with a modeled xylem sap flow profile [1]. In this study, we also employed the HFD method to measure sapwood depth at 1 cm intervals up to 7.5 cm. The light transmittance method yielded an average sapwood depth of 2.7 ± 0.6 cm, which is consistent with the literature values. However, HFD measurements revealed xylem sap flow extending to an average depth of 5.5 cm with a logarithmic decline. When calculating whole-tree water use, the light transmission plus modeling approach underestimated daily water consumption by 20.0 ± 0.3 % compared to the HFD approach. Our results demonstrate that visual determination of sapwood depth can be misleading, leading to a severe underestimation of water use at both the single-tree and stand level. As the slope of the xylem sap flow profile is additionally influenced by weather conditions and abiotic stress intensity [2], we strongly recommend incorporating such measurements into future studies on forest water relations.

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3B: Ozone uptake and Ozone-Induced Oxidative Stress: A Comparative Study of Urban Tree Species on a hot summer day

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Tropospheric ozone (O_3) is a greenhouse gas and pollutant that induces oxidative stress in plants, leading to cellular damage and altered metabolism. Its impact varies by species, influenced by stomatal conductance, assimilation rates, and antioxidant defenses. This study examined five urban tree species in Central Europe – *Fagus sylvatica*, *Pinus sylvestris*, *Quercus robur*, *Quercus rubra*, and *Robinia pseudoacacia* – under short-term ozone exposure (120 ppb). *Quercus robur* showed high sensitivity with reduced photosynthesis, while *Pinus sylvestris* displayed resilience due to strong antioxidant defenses. *Robinia pseudoacacia* had the highest stomatal ozone uptake, suggesting limited short-term acclimatization, while *Fagus sylvatica* showed lower uptake than expected. Ozone exposure also affected secondary metabolites, increasing caffeic acid and quercetin in *Fagus sylvatica* and flavones in *Robinia pseudoacacia*. These findings highlight species-specific ozone responses and their ecological implications.

3C: Natural variation in drought sensitivity and associated metabolome under soil drying in European black pine (*Pinus nigra* Arnold s.l.)

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European black pine is an ecologically and economically important tree species. Due to its high drought tolerance, it has been proposed as a candidate for assisted migration in Central European forestry. However, little is known about natural variation in drought sensitivity and associated metabolic adaptations to drought at the seedling stage in black pine. We applied automated high-throughput phenotyping to assess natural variation in drought sensitivity across nine black pine populations, and integrated targeted and untargeted metabolomics to investigate associated metabolic signatures in a subset of contrasting populations. Our results revealed significant variation in drought sensitivity among black pine populations. Climate–trait associations showed a weak, marginally significant correlation between aridity index and drought sensitivity. To investigate the metabolic basis of this variation, we selected four provenances (two tolerant, two sensitive). Targeted analysis confirmed known drought-related metabolites, whereas untargeted metabolomics showed that sensitive and tolerant populations clustered separately based on their metabolic profiles, indicating distinct drought-response strategies. Overall, our study reveals substantial natural variation in drought sensitivity among black pine populations, which is associated with distinct metabolic profiles. The putative metabolites underlying distinct metabolic profiles offer promising candidates for future screening across broader populations or related conifer species.

3D: The Road Taken Makes All the Difference: Order-Dependent Molecular Acclimation of *Pinus pinaster* to Heat and Drought Stress

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When heatwaves and extremely dry soil conditions occur at the same time, there is often a huge negative impact on ecosystems and forests. In recent years, significant research has focused on understanding how trees respond to combined drought and heat stress. Still, one of the questions often overlooked is, whether the stress-sequence imposition of drought and heat alters the molecular response to combined stress. For this purpose, we carried out an integrated metabolomic and proteomic analysis of the heat-drought (HD) and drought-heat (DH) combined acclimation responses in two slightly geoclimatically different *Pinus pinaster* provenances. The results showed that the order of stress exposure clearly influenced physiological and molecular acclimation profiles. When seedlings are first exposed to drought (DH), stomata closure results in starvation cellular context that promotes protein autophagy, shown by an increase in metabolites associated with amino acid metabolism (dipeptides and free amino acids). However, initial high temperature exposure (HD) delays this starvation by allowing longer carbon assimilation through the stomata, affecting the availability of resources for the synthesis of secondary metabolites that could participate in protection against oxidative stress and cellular damage throughout the stress acclimation process. We conclude that the order of stress exposure seems to lead to different metabolomic and proteomic acclimation profiles, and that the combined responses are modulated differently in different maritime pine provenances.

3E: Physiological responses of holm oak (*Quercus ilex* L.) seedlings to biotic stress and eco-friendly mitigation strategies for forest decline

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Holm oak (*Quercus ilex* L.) is a keystone species in Mediterranean forests, where it plays a fundamental role in sustaining biodiversity, ecosystem services, and rural economies. However, *Phytophthora cinnamomi* is increasingly threatening the resilience of these ecosystems by causing root rot and contributing to widespread tree decline. This study focuses on the physiological responses of holm oak seedlings to biotic stress caused by *P. cinnamomi* and explores how these responses can be modulated by sustainable biostimulant-based treatments. We assessed photosynthetic activity, stomatal conductance, chlorophyll fluorescence, and water potential as key indicators of plant performance under pathogen pressure. Two mesocosm experiments were conducted to evaluate how different eco-friendly treatments—ranging from mycorrhizal fungi and Plant Growth Promoting Rhizobacteria (PGPR) to biofertilizers—affect physiological resilience in infected seedlings. Among the tested treatments, Kalex Evo, Tricoten, and Bactrium notably mitigated the negative effects of pathogen infection, maintaining higher photosynthetic efficiency and water-use balance. Their combined application revealed synergistic effects on physiological parameters, indicating enhanced plant stress tolerance. This is the first study to provide an in-depth physiological characterization of holm oak responses to *P. cinnamomi* under the influence of bio-based treatments. The results offer valuable insights into host–pathogen interactions and highlight the potential of physiological markers for monitoring plant health in sustainable forest management practices.

4A: PANOMICS – a paradigm shift in plant biolog

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Due to advancements in genome sequencing, pan-genomics technology is rapidly developing, enabling comprehensive intra-specific genome-wide comparisons [1]. However, while pangenomes provide valuable genetic insights, they often fall short in identifying functional biomarkers, prompting the rise of pan-transcriptomics, which expands analysis beyond DNA sequences [2]. It is obvious that all these analyses will not stop at the DNA or RNA level but continue to integrate further level along the central dogma of molecular biology: proteomics and metabolomics, merging in the concept of PANOMICS [3,4]. The concept of PANOMICS is to integrate fundamental techniques of systems biology such as genomics, RNAseq, proteomics and metabolomics with intra- and inter-specific variation of large germplasm collections [4,5]. In my talk I will introduce examples for panomics data integration and strategies to implement this in future crop breeding [6].

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4B: Diverse adaptive responses to heat and drought in the climate-resilient crop *Camelina sativa*

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Climatic variability and extreme weather events are having an increasing impact crop yield and value. *Camelina sativa* is an old, low-input Brassicaceae oilseed crop valued for its high-quality seeds and its adaptability to a wide range of climate conditions. Camelina's innate resilience to abiotic stress offers an opportunity to uncover stress tolerance mechanisms and explore crop plasticity important for breeding climate-tolerant oilseeds. Within the project UNTWIST (www.untwist.eu), 54 camelina accessions were collected from across Eurasia to assess the genetic and physiological diversity of camelina in response to drought and heat. Genome sequencing and population structure analysis showed that the study panel captured the diversity observed in the larger publicly available population. To investigate the multilayered responses to drought and heat stress of individual camelina biotypes, a combination open field trials and trials in controlled environment was used. Camelina demonstrated resilience to heat and drought and the population exhibited a range of different adaptive responses. Morphology and phenology showed contrasting responses to each stress. (Un)targeted metabolomics profiling revealed a reorganization of metabolism, with substantial variation in line-specific responses to each of the applied stresses. The same trend was found in leaf fatty acid composition remodeled by stress. The systems approach to dissect the cellular stress response are now used for mechanistic and predictive models as well as for developing robust markers for crop performance for variable environments.

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4C: Cellular Redox Status and Carbohydrate Metabolism in the Old Oilseed Crop Camelina under Drought and Waterlogging Stress

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Extreme weather events such as prologued droughts or heavy precipitations are becoming more frequent due to climate change, threating the global food security. Therefore, there is a pressing need to develop robust crops and sustainable farming methods. *Camelina sativa*, a Brassicaceae oilseed crop with high-quality seeds, is valued for its adaptability to a variety of climatic conditions and represents a viable option for sustainable oilseed production in the face of climate change [1]. Camelina is a versatile, but underutilized crop with different cultivars and landraces originating from diverse climatic and geographical zones, differing in their breeding history and degree of stress tolerance. This study investigates cellular redox status and carbohydrate metabolism in camelina plants grown under drought and waterlogging conditions. These metabolic pathways are crucial for plant survival under stress and for efficient energy reallocation. Previous research in our group has demonstrated that profiling carbohydrate enzyme activities in response to salt stress allows the identification of specific activity signatures associated with differences in yield stability [2]. This study investigates the dynamic changes in cellular redox status and activity pattern of key carbohydrate enzymes in response to limiting and excess water. The knowledge gained can contribute to developing improved camelina varieties with enhanced climate change resilience and provide valuable insights into plant stress response mechanisms that could be applied to other crops.

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4D: Exploring drought-induced metabolic changes in montane conifers

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Mountain ecosystems are affected by increasingly more extreme climate events, including droughts. However, the biochemical pathways underlying drought resilience in montane conifers remain unclear. Here, we compared needles from 2-year-old *Pinus sylvestris* (scots pine) and *Juniperus communis* (common juniper) plants exposed to mild, moderate or severe drought to those of non-stressed saplings, under controlled conditions, using untargeted GC-MS-based metabolite profiling, and targeted LC-MS/MS and HPLC analyses of hormones, antioxidants and lipid peroxidation markers. In juniper, drought induced an increase in osmoregulatory sugars and proline, and seven organic acids, including four TCA cycle intermediates, but a decrease in citrate, cis-aconitate and glycerate. Pine predominantly accumulated amino acids, including serine, leucine and γ--aminobutyrate. In both species, concentrations of indole-3-acetic acid, gibberellic acid, glutathione and glutathione disulphide rose with increasing drought intensity, and lipid peroxidation markers, including hexaldehyde, trans-2-hexenal and 4-hydroxyhexenal, under moderate (pine) or severe drought (juniper). Abscisic acid peaked at moderate drought in juniper and progressively increased in pine, while jasmonic acid concentrations declined in pine, and salicylic acid in juniper. Whereas lipid peroxidation products, indicative of oxidative stress, were observed in both conifers, species-specific differences in drought responses included enhanced osmotic regulation and modification of organic acid metabolism in juniper, and accumulation of amino acids in pine. The observed species-specific differences suggest that resilience to drought is subject to complex, differential metabolic regulation. Further effects of the downstream consequences for tree health, including potential increasing vulnerability to pathogen attack, are discussed.

4E: Crops in a changing climate environment – a MULTIOMICS perspective

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The food demand in the world is growing due to the increasing population and decreasing availability of agricultural land, which requires new crops that are more productive and resilient to harsher environmental conditions. Thus, rapid and effective exploration, identification, and validation of an important trait, gene, molecular mediator, and protein interaction are important for improving crop yield and quality in the near future. Integrating genomics, transcriptomics, proteomics, metabolomics and phenomics enables a deeper understanding of the mechanisms underlying the complex architecture of many phenotypic traits of agricultural relevance. Additionally, the high-resolution proteomics technologies necessitated a gradual shift from the general descriptive studies of plant protein abundances to large-scale analysis of protein-metabolite interactions. Especially, advent in metabolomics is currently receiving special attention, owing to the role metabolites play as metabolic intermediates and close links to the phenotypic expression [1-3]. In this context, I present a case study on important legume such as chickpea which highlights drought-responsive metabolite markers such as L-threonic acid, fructose and sugar alcohols that are involved in chickpea adaptive drought response within the mid-pod-filling stage. We performed SSI (stress susceptibility index) that distributed 36 genotypes into four categories from best to worst performance under stress condition. These genotypes can be explored for breeding chickpeas under stress [4]. Metabolic GWAS (mGWAS) analysis uncovered gene candidates involved in glycolysis and MEP pathway corroborating with the differential biochemical Jacobian results. Accordingly, this proposed data analysis strategy bridges the gap from pure statistical association to causal biochemical relations by exploiting natural variation. Our study offers new perspectives on the genetic and metabolic understanding of drought tolerance-associated diversity in the chickpea metabolome and led to the identification of metabolic control points that can be also tested in other legume crops [4]. Integrating the OMICS approach to modern plant breeding and genetic engineering methods ensures the development of climate-smart crops with higher nutrition quality that can sustainably meet the current and future global food demands [1-3].

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5A: Biochemical Adaptations of Tomato Plants (*Solanum lycopersicum* L.) in Response to Environmental Stress and Biotic Interactions

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The tomato (*Solanum lycopersicum* L.), a widely cultivated member of the Solanaceae family, contains bioactive compounds such as phenols and amino acids, whose concentrations are influenced by environmental conditions. Climate change, particularly increasing temperatures and biotic and abiotic stress factors, significantly affects tomato growth, physiology, and biochemical composition. This study investigates the influence of environmental conditions on the metabolite profile, including antioxidants, sugars, and organic acids, in seven tomato varieties. Seven tomato varieties, previously assessed for visual and taste characteristics in 2018 and 2019, were grown under standardized climatic and soil conditions at a single location. Harvested fruits were analyzed using high-performance liquid chromatography (HPLC), ion exchange chromatography (IC) and photometric methods. Results demonstrated year-to-year variations in key metabolites. In 2018, malic acid concentrations ranged from 0.29 to 1.47 mg/100 mg dry weight (DW), citric acid from 3.44 to 7.32 mg/100 mg DW, and glucose from 16.24 to 25.22 mg/100 mg DW. In 2019, these values exhibited broader fluctuations: malic acid (0.05–2.41 mg/100 mg DW), citric acid (0.46–10.00 mg/100 mg DW), and glucose (1.85–23.20 mg/100 mg DW). The observed interannual and varietal differences highlight the significant impact of genetic and ecophysiological factors on tomato metabolite composition. Climate-induced stressors can not only alter yield but also substantially modify the concentration of tomato-specific bioactive compounds, emphasizing the need for adaptive breeding and cultivation strategies in the face of climate variability.

5B: Investigating the Role of Calcium-Dependent Protein Kinases in Potato Tuber Formation

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Potato tuberization is a complex process regulated by biochemical, genetic, and morphophysiological factors. The florigen homolog StSP6A, induced under short-day photoperiods and low temperatures, plays a central role. Transported from leaves to stolons, StSP6A interacts with 14-3-3 proteins and phosphorylated bZIP transcription factors to form the tuberigen activation complex (TAC), essential for tuber initiation. Cytosolic Ca^{2+} signals regulate plant development, particularly via Ca^{2+}-dependent protein kinases (CDPKs). Arabidopsis studies suggest CDPKs phosphorylate bZIPs, likely mirroring potato mechanisms. However, Ca^{2+}-mediated tuberization pathways remain poorly understood. To identify TAC-associated CDPKs, we aligned Arabidopsis CDPKs with Solanum tuberosum homologs, analyzed conserved phosphorylation domains, and screened candidates for phosphorylation sites. Five StCDPK isoforms were selected for in vitro kinase assays on group A StbZIPs. Among them, StCPK17 exhibited the highest phosphorylation efficiency. Co-immunoprecipitation (Co-IP) confirmed its interaction with key StbZIPs. Field trial data from ADAPT collaborators further identified CPK17 as a prime candidate for tuberization regulation. StCPK17 is a strong tuberigenic signaling candidate due to its high phosphorylation activity. In vitro potato culture under tuber-inducing conditions showed calcium availability directly influences tuber initiation. EGTA and $LaCl_3$ treatments inhibited tuber formation, confirming Ca^{2+}'s role. These results position CPK17 as a key regulator of tuberization, mediating phosphorylation events essential for TAC formation.

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5C: Role of HDA9-HDA19-HAT3 repressor complex during dehydration stress in C_4 model crop foxtail millet [*Setaria italica* L.]

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Climate change imposes multiple stresses on plants, with dehydration stress significantly affecting growth and productivity. Foxtail millet (*Setaria italica*), a C_4 panicoid crop, serves as an excellent model for studying dehydration stress. However, the role of epigenetics in regulating dehydration stress-related genes remains unexplored. The acetylation of lysine residue 9 of histone H3 (H3K9ac) is a key epigenetic mark, dynamically regulated by histone acetyltransferases (HATs) and histone deacetylases (HDACs) [1]. Chromatin immunoprecipitation (ChIP) assays showed differences in H3K9ac patterns between control and dehydration-stressed samples. RNA-sequencing and qRT-PCR confirmed differential expression of histone modification genes. A histone deacetylase, SiHDA9, was significantly upregulated in the sensitive cultivar. Interaction studies revealed that SiHDA9 forms a repressor complex with SiHAT3.1 and SiHDA19. Virus-Induced Gene Silencing (VIGS) assays showed that silencing SiHDA9 upregulated key dehydration-responsive genes (SiRAB18, SiRAP2.4, SiP5CS2, SiRD22, SiPIP1;4, SiLHCB2.3), enhancing dehydration tolerance. [2]. SiHDA9 is likely recruited through SiHAT3.1 to dehydration-responsive genes, reducing H3K9 acetylation and repressing their expression. The formation of the SiHDA9-SiHAT3.1-SiHDA19 complex under dehydration stress establishes a regulatory mechanism that impacts stress tolerance. This study highlights the critical role of histone acetylation in dehydration tolerance and provides mechanistic insights into how SiHDA9 negatively regulates stress responses in foxtail millet, offering potential targets for enhancing crop resilience [2].

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5D: Investigating the unique attributes of the European bilberry on natural stands: implications for cultivation and regional value creation

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The European bilberry (*Vaccinium myrtillus* L., Ericacea) is a small shrub indigenous to Europe, including Alpine and Carpathian regions. It is differing significantly from its American relatives. This study delves into Austrian provenances of *V. myrtillus* examining diversity in phenotyping and biochemical traits. Focused on Austrian bilberry, our research encompassed characterization of eco-physiological site factors, analysis of diversity among populations, and an exploration of in vitro and horticultural cultivation possibilities. This study analyzed seven natural sites in Austria, assessing factors like soil conditions, biological and morphological variability, and plant morphology. The Austrian bilberry exhibits significant within-population diversity, crucial for its adaptation and survival in diverse environments. Environmental conditions across various sites notably influence plant morphology. Pathogenesis-related proteins enhanced our understanding of the plant's defense mechanisms and allergenic potential. Preliminary anthocyanin measurements indicate substantial nutritional and health-related potential. In vitro cultivation presents a promising method for propagating the species, considering its complex genetic traits and high demand for its health-beneficial compounds. This study sheds light on its ecological, genetic, and biochemical complexity, highlights the species' potential as a valuable natural resource for nutritional and pharmaceutical applications and the findings pave the way for agricultural innovation and biotechnological advancements in sustainable berry cultivation. Domesticating bilberry for regular farming in nurseries or on marginal or remote sites appeared promising (e. g. after clear cutting) having a potential of creating an additional source of revenue.

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6A: Early response to nickel on root growth, cell wall alteration and THESEUS1 dependent phosphoregulation

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The plant cell wall serves as a first barrier against environmental stresses in plants and initiates rapid defense response. These early events trigger downstream signaling and adaptive mechanism for plants to survive. In this study, we investigate the immediate effects of increased nickel (Ni^{2+}) concentration on root meristem activity, cell wall remodeling and phosphorylation mediated by the cell wall integrity sensor THESEUS1 (THE1). Time-dependent Ni^{2+} exposure response revealed a dynamic oscillating pattern in root meristem activity. To understand effect of Ni^{2+} in cell wall components generally functioning for cell expansion, we quantified changes of pectin methylesterase (PMEs) activities that are induced within 2 hours in a dose dependent manner. Time-resolved phosphoproteomics analysis identified 32 phosphoproteins with altered phosphorylation status within 5 min of Ni^{2+} exposure, peaking at 45 phosphoproteins by 30 min. To find out Ni^{2+} triggered and THE1 dependent phosphoproteins, these results were integrated with phosphoproteomic profiling of the knock-out mutant *the1-6*. To sum up, our research shows fast and dynamic changes upon Ni^{2+} exposure and the involvement of THE1 for these adaptive responses.

Acknowledgements

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6B: KIN10 is Required to Orchestrate Efficient Cell Elongation in Response to Pathogen Attack and Light

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KIN10, the catalytic subunit of SnRK1 (SUCROSE NON-FERMENTING RELATED KINASE 1) is a key regulator of plant energy homeostasis and stress responses. While its role in metabolism is well established, its function in cell elongation remains unclear. Therefore, we are applying a holistic approach integrating transcriptomics, metabolomics, and cell biology to investigate KIN10's role in regulating root and shoot elongation processes triggered by abiotic and biotic stimuli. RNA sequencing, mass spectrometry, and high-resolution live imaging were used to analyze KIN10 mutants and overexpressors under pathogen attack and changing light exposure. Root elongation, root hair formation, and hypocotyl growth were quantified to decipher KIN10's role in cell expansion. KIN10 is crucial for coordinated cell elongation in both roots and shoots. *kin10* exhibited reduced root elongation under pathogen stress but unaffected root hair development. In hypocotyls, *kin10* displayed impaired elongation under light exposure [1], linking KIN10 to photomorphogenesis regulation. Hormonal profiling showed increased stress responses in *kin10* roots, indicating a trade-off between defense and growth. Transcriptomic analysis confirmed that KIN10 orchestrates jasmonic acid and salicylic acid signaling, while its absence suppresses these pathways. Reduced reactive oxygen species (ROS) accumulation in *kin10* seedlings suggests impaired ROS-mediated signaling in cell expansion. KIN10 integrates metabolic and hormonal signals to fine-tune cell elongation in response to biotic and abiotic stimuli. Our findings highlight the broader role of SnRK1 in balancing growth and stress adaptation.

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6C: Plant resilience at the molecular level: How protein modification helps to withstand stressful conditions

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Protein modification by the small modifier proteins ubiquitin or SUMO (small ubiquitin-related modifier) is frequently an early step in signaling of stressful conditions. We study these two modifications in the model plant Arabidopsis. We analyze a ubiquitin-dependent pathway that helps plants to withstand flooding. Flooding causes oxygen shortage (hypoxia), which slows down growth and induces genes that change metabolism from respiration to fermentation. These changes are induced by transcription factors that are quickly degraded under normoxic conditions, but that are stabilized by lack of oxygen. The degradation depends on an amino-terminal degradation signal contained in these transcription factors that requires oxidation for full activity. The oxidation step makes covalent addition of ubiquitin dependent on oxygen concentration. Ubiquitin in turn is the signal for proteolytic destruction of the target proteins. We also investigate steps of covalent SUMO linkage to substrate proteins. Decreased ability to carry out this modification causes increased sensitivity to heat, cold and salt stress. We analyze mutants that are deficient in different steps of the conjugation pathway. Of specific interest is a group of enzymes called SUMO-dependent ubiquitin ligases. We are currently generating double and triple mutants that lack more than one enzyme of this group. We investigate how mutations in these enzymes change salt (NaCl) sensitivity. The group of so-called 14-3-3 proteins are substrates for the SUMOylation pathway. 14-3-3 proteins can bind to phosphorylated Tyr or Ser residues on proteins as so-called “readers” of phosphorylation marks deposited by protein kinases during development or in response to stresses. 14-3-3 binding orchestrates changes necessary for developmental transitions, or for adaptation to new external conditions. 14-3-3 proteins are known to function in transcription and enzyme regulation. We want to understand the role of SUMOylation in these processes. We analyze whether a potential role of 14-3-3 proteins in heat stress response is modulated by conjugation to SUMO.

6D: proximity labelling enters plastids

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Plastid developmental transitions often happen in narrow time spans and spatially restricted areas within plants. This limits experimental accessibility by classical biochemical techniques to study spatiotemporal protein environments in such transition processes. To overcome this problem, we developed a TurboID-based proximity labelling workflow that requires only very limited sample amounts to obtain mechanistic insights into protein interaction networks present during these transition stages. We used the AtCGL20a protein, a factor described in chloroplast development, as bait for in vivo proximity labelling in developing seedlings. In agreement with its previous hypothesised function, we find it residing in a nexus of RNA binding proteins. Unexpectedly, we noticed that TurboID also retains part of its activity as preprotein prior and during import into the plastid. We even observe differential enrichment of certain TOC/TIC components depending on the peptide sequence of the imported protein despite harbouring the same plastid targeting peptide. These enrichment data can be interpreted as "residence time differences" of the respective preprotein next to individual components of the TOC/TIC import complex. Therefore, we suggest that TurboID based proximity labelling can be a useful tool to study dynamics of plastid protein import in vivo.

6E: An integrated database of antiglycan monoclonal antibodies based on a complex meta-analysis of published data

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Studying plant cell walls is highly challenging due to their high heterogeneity and complexity. The monoclonal antibodies (mAbs) have been a valuable tool for decades to detect/visualize glycan epitopes directly in situ or for high throughput profiling of cell wall-derived samples. Despite their popularity, one of the ongoing issue is the low level of their characterisation which may lead to erroneous or oversimplified conclusions. Here we present a metanalysis of already published data on antiglycan monoclonal which we integrated into a searchable database. Using the statistical methods, we reanalysed the obtained data, depicting the epitopes in conventional symbol system and organized all the information into clear and user-friendly web page that will be accessible online. In future, we intent to enhance the user interface and enrich it with new experimental and in silico data. This new data resource integrates the so far unorganised knowledge on anti-glycan mAbs, and can help the researchers in their choice making and for better utilisation of cell wall-directed probes.

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7A: Exploring the role of HIPP proteins in regulating auxin responses

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Auxin is a key plant hormone that orchestrates growth and development through AUXIN RESPONSE FACTORS (ARFs); transcription factors that mediate auxin-induced gene expression. Our research uncovers a novel regulatory layer involving intrinsically disordered HEAVY METAL-ASSOCIATED ISOPRENYLATED PLANT PROTEINS (HIPPs), which interact with ARFs and are necessary for the transcriptional responses to auxin. HIPPs are plant-specific proteins of largely unknown physiological function. Our research revealed that a group of phylogenetically closely related HIPP proteins from Arabidopsis form biomolecular condensates and that they play an important role in regulating various developmental processes. Transcriptomic analysis of *hipp* loss-of-function mutants revealed widespread alterations in auxin-responsive gene expression. Protein interaction studies further demonstrated that HIPPs associate with multiple ARFs, with these interactions occurring in cytoplasmic biomolecular condensates. Our findings indicate that HIPPs regulate the stability of ARF proteins and their nucleo-cytoplasmic partitioning, thereby modulating auxin signaling. Importantly, we show that the HIPP-ARF interactions are biologically significant, as they are crucial for auxin- dependent developmental processes, including lateral root formation. We will discuss our findings and recent advances toward elucidating the molecular mechanism by which HIPP proteins regulate auxin responses.

7B: Complex Speciation in Crataegus: Unraveling Hybridization, Polyploidy, and Apomixis in Central Europe

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Hybridization, polyploidization, and apomixis are evolutionary forces that blur species boundaries diversity in the genus *Crataegus*. In Central Europe, diploid sexual species (e.g., *C. monogyna* and *C. laevigata*) coexist with the predominantly polyploid apomict *C. rhipidophylla*, leading to natural hybridization events. We sampled leaves and fruits from ten populations and employed a combination of nuclear microsatellite genotyping, flow cytometry, and morphological analyses of leaves and fruits. This integrative approach allowed us to distinguish parental species from hybrids and assess their reproductive modes. Genetic clustering delineated clear parental lineages with evidence of geographic structuring in *C. laevigata* and *C. rhipidophylla*. While morphological traits effectively separated the parental species, hybrid forms exhibited overlap. Flow cytometry revealed that the diploid hybrid *C.* × *media* reproduces sexually, whereas hybrids involving the polyploid parent reproduce via apomixis. These findings underscore the critical role of ploidy in governing reproductive strategy and highlight the challenges of species delimitation in groups affected by hybridization and polyploidy. Our study demonstrates that an integrative taxonomic framework combining genetic, morphological, and cytological data is essential for understanding the speciation continuum within the complex *Crataegus* group.

7C: Phenotypic and Chemical Cuticle Plasticity in *Kalmia procumbens*

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Kalmia procumbens, an alpine dwarf shrub thriving at high elevations, exhibits remarkable cuticle structural and chemical plasticity, indicative of environmental acclimation. Plants growing on north- and southeast-facing slopes developed distinct cuticle characteristics, with southeast-facing leaves exposed to extreme environmental conditions forming thicker cuticles (16 µm) than north-facing leaves (11 µm). Raman micro-spectroscopy and multivariate analysis revealed a complex layered cuticle composition including cutin, triterpenoids (amyrins, ursolic, and oleanolic acid), and phenolic compounds such as flavonoids and cinnamic acids (Fig. 1). Flavonoids impregnated the outer adaxial cuticle layer, with higher concentrations in north-facing leaves, where they likely contribute to pathogen (fungi) defence. However, the flavonoid enrichment appears to increase water permeability (gmin), leading to significantly higher water loss above 38 °C compared to the thicker southeast-facing cuticles, which maintained lower gmin. Alkanes were detected as thin layers in the cuticle and at the base of trichomes, while triterpenoids displayed variable distribution and composition. Specifically, amyrins were present on the abaxial cuticle, while ursolic and oleanolic acid impregnated the adaxial cuticle and distal regions of trichomes, suggesting a protective role against heat stress. These findings integrate ecological, structural, and microchemical insights, and illustrate how alpine microhabitats drive phenotypic and functional leaf cuticle acclimative responses in *K. procumbens*. The multi-layered, thick cuticle structure, enriched with specialized chemical compounds, exemplifies a finely tuned strategy to balance water retention, pathogen defence, and environmental resilience in extreme alpine ecosystems.

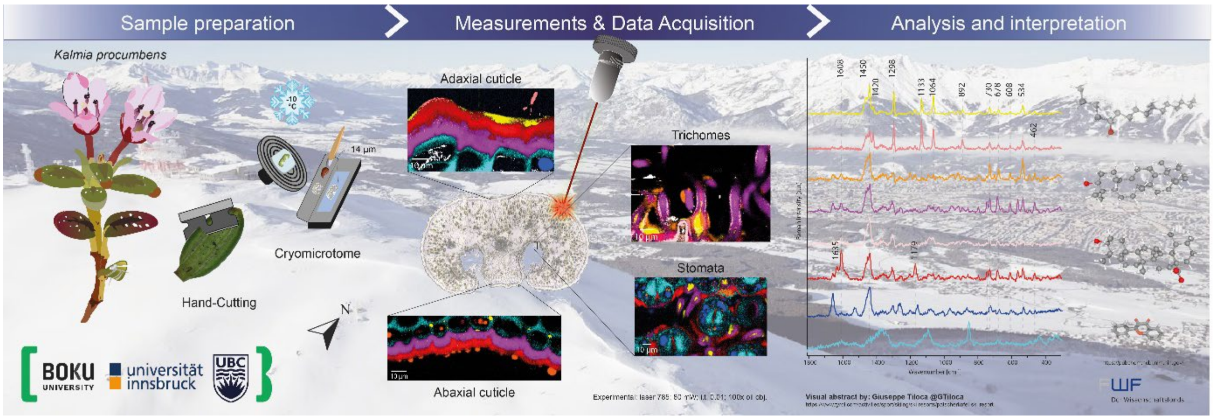

Figure 1 Overview of the Raman imaging workflow, from sample preparation (left) to measurements (middle) and final analysis and interpretation (right). The background image features Mt. Patscherkofel (Innsbruck, Austria), where *Kalmia procumbens* branches were collected from both north- and southeast-facing slopes. For sample preparation, leaf micro cross-sections (14 µm) were cut using a cryo-microtome, mounted on a standard glass slide with a drop of distilled water, and sealed with nail polish. Hyperspectral datasets were acquired with a Confocal Raman Microscope (785 nm, 80 mW, 0.1 s). Raman images and average spectra across the leaf surfaces were generated using True Component Analysis in WITec Control 6.0 (Oxford Instruments). Spectral interpretation and band assignments were based on literature references and validated with measured reference samples.

7D: Root-derived cytokinin regulates flowering time in *Arabidopsis thaliana*

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Transitioning from vegetative to reproductive development is a critical phase in a plant's life cycle, significantly impacting its reproductive success. In addition to the previously established components in the gene regulatory network controlling flowering time, the phytohormone cytokinin has been discussed as another possible factor. However, the underlying molecular mechanisms and interconnection with the known flowering pathways have remained elusive. We could show which cytokinin metabolism and signaling genes regulate flowering time and revealed that cytokinin promotes flowering independently of the photoperiod and plastochron. Notably, abrogated CK export from roots and reciprocal grafting experiments highlighted the importance of root-derived cytokinin as a key flowering signal. Additionally, our gene expression studies and genetic analyses uncovered a functional link between cytokinin and the age pathway, characterized by the antagonistic expression of microRNAs miR156 and miR172, which target various SQUAMOSA PROMOTER BINDING LIKE (SPL) and APETALA2 (AP2)-like transcription factors. This link highlights the role of different components of the age pathway downstream of cytokinin signaling, providing a deeper understanding of the complex regulatory network that controls plant reproductive development.

7E: Exploring heavy metal localization in mosses using nanoscale x-ray imaging

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The accumulation and distribution of heavy metals within plant tissues are of great interest for phytoremediation and environmental biomonitoring [1]. Bryophytes are frequently used to assess environmental pollution due to their ability to absorb essential minerals and water, as well as harmful heavy metals, throughout their entire surface [2]. In this study, we present some results of an advanced analysis conducted at NanoMAX synchrotron (MAX IV; Lund, Sweden), an X-ray beamline for imaging and diffraction studies at the nanoscale. Our aim was to localize and quantify the presence of Cu and Fe, alone and in combination, within the tissues of two moss species: *Physcomitrium patens* and *Pohlia drummondii*. Moss specimens were cultivated under controlled conditions on a medium contaminated with Cu and Fe (100 µM) for four weeks. The samples were dehydrated by the freeze-drying with liquid nitrogen. In this process, the samples were placed inside aluminum foil containers, immersed in liquid nitrogen for a few minutes, and then transferred to the freeze dryer (Leica EM MED 020) for 24 h to ensure the complete removal of water without altering or damaging the cell structure. The results highlight differences in metal accumulation and distribution between the two species. Synchrotron radiation techniques, particularly X-ray imaging and diffraction, enable high-resolution analysis of metal localization within plant tissues. This advanced approach enhances our understanding of metal uptake and retention mechanisms in mosses, providing valuable insights into their strategies for coping with metal-induced stress [3].

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8A: Fatigue cracks in trees and walnuts

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Cyclic loading can cause fatigue cracks and failure at far lower stress levels than the strength of the material. Crack initiation and crack propagation are longtime not seen until the material fails. But how is nature mitigating fatigue, and is it always bad? Here we present two plant systems: the wood tissue of trees that rely on the prevention of fatigue and the suture tissue of walnut shells that open upon repeated loading. Trees are exposed to cyclic loads, mainly by wind, causing the stem to bend back and forth. Under compression, cell walls kink close to the boundary between early and late wood, leading to buckling of early wood tracheids [1]. Under tension, these creases initiate cracks, which propagate with each loading cycle [2]. These mechanisms have been observed during experiments on wood samples. However, trees are continuously growing throughout their lives by adding new cell layers each year. We explore experimentally, if the addition of new cell wall material can counteract kink formation and protect the wood tissue from fatigue. Contrary to the trees, nuts possess a protective tissue made up of dead sclerified cells that withstand high compression forces [3]. Though, walnuts have additionally a pectin-rich suture tissue that allows the shell to open under conditions suitable for seed growth. Both tissues expand and shrink differently under changing humidity levels, generating perpendicular forces at the interface [4]. We show that under cyclic humidity changes, fatigue cracks are initiated and propagate along the suture tissue, enabling the seed to split the shell during germination.

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8B: 3D Multimodal Image Registration for Plant Phenotyping

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Multimodal vision systems are increasingly used in plant phenotyping to combine data from different imaging technologies, such as RGB, thermal or hyperspectral cameras. The combination of different imaging technologies can enable deeper insights into plant health and structure. However, combining images from multiple modalities poses challenges due to variations in camera placement and lens characteristics, which result in non-aligned images. We propose an image registration approach that incorporates depth information to address alignment issues in multimodal setups. Unlike conventional 2D-only registration methods, our approach leverages 3D geometry to improve accuracy and reduce errors related to occlusions [1]. The method achieves improved pixel alignment across modalities by using depth cues to guide registration. It also includes an automated process for detecting and excluding occluded regions, which enhances the reliability of the final registered outputs. By integrating depth data and occlusion-aware filtering, the proposed approach overcomes significant limitations of traditional 2D-based registration. This enables more accurate cross-modal analysis and supports more robust phenotypic assessment in complex plant structures. Depth-based multimodal registration improves the alignment and interpretability of image data in plant phenotyping systems. The technique contributes to more precise and reliable multimodal analyses, advancing the capabilities of plant imaging technologies.

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8C: Multi-scale Characterization of Cotton Fiber Structure and Properties

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The seed hairs of cotton are the most widely used plant fibers for clothing, home furnishings, and industrial products.[1] The utilization of cotton fibers to generate high quality yarn for textile applications depends on multiple fiber characteristics, including fiber length, fiber twists, and the fibers´ mechanical properties. Cotton fibers mechanics are highly dependent on the cell wall thickness and the properties of cotton cellulose (arrangement, angles and other characteristics of the highly crystalline cellulose fibrils).[2,3] This study focuses on the structure of *G. hirsutum* fibers in a multi-scale approach including light and electron microscopic techniques, vibrational spectroscopy, and wide-angle X-ray scattering. Micromechanical tensile tests are performed to reveal the relationships between tensile behavior and determined structural features. Additional experiments are introduced to investigate the influence of changing environmental humidity on cellulose crystals, fiber morphology, and the associated behavior of individual cotton fibers. The experiments revealed the complexity of the cotton fiber cell walls and their broad influence on the fibers´ mechanical properties. Significant differences in cell wall-specific characteristics and mechanical functionality were observed in relation to the examined fiber region. In a correlative approach, the alignment and angle of cellulose fibrils were determined. WAXS measurements at the synchrotron facility BESSY II in Berlin revealed the effect of external humidity changes on cotton cellulose. The findings of this project facilitate a deeper understanding of the property-function relationships within cotton fibers. This underscores the interconnectivity of the hierarchical structure and the mechanical properties for which cotton is known and widely utilized.

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8D: How conifers and grasses overcome physical limits to sugar export from leaves

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Plants export much of the sugar produced by photosynthesis from leaves to carbon sink organs, where they fuel growth and development. The sugar export rate is influenced by various factors, including intracellular sugar metabolism and transport, intercellular water flow, inter-organ sugar gradients and cell anatomies. Understanding how these factors combine to adjust sugar export according to growth strategy and environmental conditions requires quantitative data. The relatively simple structure of conifer needles enabled us to generate such data. Theoretical modeling of sugar and water flows in conifer needles based on anatomical data from a range of species indicated a strongly reduced sugar export efficiency in tips of needles longer than 5-10 cm[1]. A surprising result, that was corroborated by our discovery of mechanisms that could overcome the physical limitation in these species. One mechanism is the channeling of sugar and water, achieved by a layered arrangement of transport conduits in the phloem vascular system. Another is the decoupling of the diurnal rhythms of carbon storage and remobilization at different leaf positions. Recently, we have explored if the parallel-veined leaves of grasses face similar structural limitations to phloem transport as the single-veined conifer needles. Especially in maize, anatomical data, sucrose transporter activities, carbon dynamics and isotopic carbon export rates indicate physical limitations to export capacity. Results will be discussed with respect to factors that shape phloem anatomy and the ecophysiological consequences of structurally constrained sugar export from leaves.

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8E: Seed sorting *via* infrared thermography reveals hidden metabolic signatures of ageing

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Understanding the molecular basis of seed ageing is crucial for developing seed viability markers of potential use in the seed trade, agriculture, and conservation. Analysing aged seed lots, containing a mixture of viable and non-viable seeds, can confound results. However, distinguishing aged-viable from aged-dead seeds prior to germination is hindered by the lack of effective separation tools. We employed infrared thermography (IRT) during a seven-hour seed imbibition period to partition pea (*Pisum sativum* L.) seeds from an aged, "unsorted" lot (UnS) into "sorted viable" (S_{viable}) and "sorted dead" (S_{dead}) sub-lots, which were then re-dried and stored. Changes in the seed metabolome were assessed using a GC-MS-based metabolite profiling approach alongside targeted HPLC and UHPLC-MS analyses of glutathione redox state and seed hormones. UnS, S_{viable} and S_{dead} seeds were compared with "non-aged" seeds (NA; all viable seeds) and "dead" seeds (D; entirely non-viable after extensive ageing) as positive and negative controls, respectively. When seeds took up water in the germination test, the abundances of distinct metabolite groups increased in NA seeds while decreasing in D seeds, or *vice versa*, with UnS seeds displaying intermediate values. S_{viable} and S_{dead} seeds exhibited diverging patterns that resembled those of NA and D seeds. Ageing-responsive metabolite levels in unsorted seeds were ambiguous, masking distinct metabolic signatures of ageing. However, IRT-based seed sorting revealed that the metabolism of S_{viable} and S_{dead} seeds reflected the distinct profiles of NA and D seeds, enabling novel insights into the mechanisms underlying seed ageing.

Poster presentations

Thursday, May 29, 2025

17:20 to 18:00	**P1- P25**

Friday, May 30, 2025

13:20 to 14:40	**free poster viewing**
18:00 to 19:00	**P26 – P50**

Please mount your poster on your assigned poster board on Thursday 12:00 to 13:00.

P1: Adaxial additional Stomata in Phylloxera-Infested Leaves: Benefit and role?

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The grapevine leaf Phylloxera (*Daktulosphaira vitifoliae*), considerably damages vine crops. It induces additional stomata on the leaf's adaxial surface in areas where it is active. Leaves from two control and Phylloxera-infected Teleki 5C grapevine plants were analyzed 50 days post-inoculation. Samples were taken from control plants and regions around the gall (PH-G) and leaf lamina away from the gall (PH-L) in Phylloxera-infested plants. The study found no significant differences in glucose, fructose, or sucrose levels between control and Phylloxera-infested plants. However, starch content was lower in infested plants, which also showed higher stomatal conductance and a higher stomatal index, with additional stomata near gall regions on the adaxial surface. The quantum yield of photosystem II remained unchanged. The results show that Phylloxera impacts stomatal formation, enhancing gas exchange while increasing water loss and energy demands. Reduced starch near gall may indicate a metabolic shift due to elevated energy use. The lower epidermal density and higher stomatal index reflect the complex changes in leaf structure caused by the infestation. It looks plant continues light-phase photosynthesis, but the Calvin cycle may be disrupted due to reduced enzyme activity or altered carbon flow. The feeding aphids consume sugars and may affect starch accumulation, forcing the plant to redirect resources for defense or photorespiration. Increased stomatal conductance leads to higher transpiration, potentially harming long-term growth. Phylloxera induces additional stomata on the adaxial leaf surface, which may initially enhance gas exchange, but they can ultimately disrupt the plant's water and nutrient balance.

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P2: Deciphering Genetic Determinants of Delayed Ripening in Grapevine through RNA-Seq Analysis

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Delayed ripening in grapevine (*Vitis vinifera*) plays a crucial role in European viticulture by enhancing fruit quality, maintaining acidity, and mitigating the impacts of climate change. This study aims to identify the genetic determinants of delayed ripening in grapevine cultivars through RNA sequencing (RNA-Seq). Transcriptome profiling was conducted on berry tissue from 12 grapevine varieties classified as early ripening (*Pinot précoce noir, Calardis Musqué*, *Madeleine royale*, *Bacchus weiss*, *Regent, Csaba gyoengye*), mid ripening (*Pinot noir*, *Dornfelder, Helfensteiner*), and late ripening (*Chardonnay blanc*, *Riesling weiss*, *Villard blanc*). Samples were collected at three developmental stages, fruit set (BBCH71), pea size (BBCH75) of berries, and beginning of veraison (BBCH81) with three biological replicates per condition, yielding a total sample number of 108. RNA-Seq was performed using the Illumina NextSeq 2000 platform, generating 1.89 billion paired-end reads in total, with an average of 17.49 million raw reads per sample. Preliminary analysis revealed differential gene expression patterns associated with ripening behavior across the developmental stages. Further variant calling and allele-specific expression (ASE) analyses are ongoing to identify genetic variants and expression profiles linked to delayed ripening traits. The findings of this study will provide insights into the transcriptional and genetic basis of ripening delay in grapevine. By elucidating key genetic factors, this research will contribute to a broader understanding of ripening regulation and provide potential avenues for improving grape quality and resilience in viticulture.

P3: Using gas chromatography and mass spectrometry (GC-MS) for the detection of drought stress effects on the metabolome of *Solanum tuberosum* varieties

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Potato (*Solanum tuberosum*) is one of the highest yielding crops in the world. Yet, the potato yield is strongly dependent on many abiotic factors. Pressuring matters like climate change urge science to understand plant stress response to abiotic factors, such as drought. This knowledge will be essential in breeding more adaptable crop varieties to maintain food security. Previous studies showed changes in plant stress-related metabolites [1,2]. Eight Potato varieties were tested on their drought response in a field trial. The samples for the analysis were collected from both irrigated (control) and non-irrigated (treatment) fields in early July 2023 in two time points. Leaf discs were grinded, and their weight normalized. Primary metabolites were targeted in the analysis by collecting the polar phase of the Methanol-Chloroform-Water extract. The metabolites were quantified and identified using Gas chromatography-mass spectrometry analysis. Further processing was done using MS-Dial and statistical analysis with R. Preliminary results indicate separation between the control and the treatment group. Between the potato varieties metabolite changes (e. g. in proline) could be measured. The differences could depend on varying conditions in the soil, the microclimate and pests in a field trial. We were able to characterize metabolic changes in *Solanum tuberosum* that are likely related to the applied drought stress conditions.

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P4: Metabolic changes of *Paraburkholderia dioscoreae* strain Msb3 on varying substrates

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Paraburkholderia dioscoreae strain Msb3 is a phyllosphere symbiont of *Dioscorea bulbifera,* that has shown great potential as plant growth promotor (PGP) [1, 2, 3]. Genes linked to PGP bacteria, including 1-aminocyclopropane-1-carboxylate deaminase (ACC deaminase) and nitrogenase, have been found in *P. dioscoreae*. ACC deaminase enables bacteria to break down the ACC, utilizing it as a source of carbon and nitrogen. Nonetheless, the way Msb3's metabolism adapts to various nutrient sources remains unclear. Previous genome based metabolic modeling showed that Msb3 has differential substrate preference, and this preference could be related to the oxygen supply. For this purpose, we carried out metabolomic (Gas-Chromatography-Mass Spectrometry, GC-MS) and growth curves analyses of different carbon and nitrogen sources that could be present in the phyllosphere, such as ACC, glucose, ammonia, malate, sucrose and tryptophan, among others. Initial results indicated that Msb3 growth varies with carbon and nitrogen sources. When growing with ACC as the sole nitrogen and carbon source, slower growth was observed compared to using NH4Cl as nitrogen source and glucose as carbon source. This growth, indicated by genome-based metabolic models, could be linked to varying availability of carbon, nitrogen, and oxygen. Msb3, which typically colonizes the leaf surface [1], especially trichomes and stomata, may favor ACC as the sole carbon and nitrogen source under high oxygen conditions. Our findings suggest Msb3's metabolic versatility adapts to oxygen availability, explaining its preference for ACC in the phyllosphere environment.

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P5: The Slow-flower movement: Contribution to sustainability in floriculture

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Flowers and cut-flowers are of importance and socio-cultural meaning in everyday's life and on special festive occasions – horticultural cultivation and florist art have a long tradition in common throughout history. Floricultural production and marketing has been consequently developing into a globalized world-wide and year-round business nowadays – floricultural supply chains are spanning over the globe connecting continents, countries and people. The “philosophy” behind: quick, colorful and cheap for brisk consumption. Looking at the problematic impacts of industrialized intensive global floriculture and its supply chains – example given on rural societies, environment and sustainability aspects - one can recognize an urge for alternatives. Currently an emerging movement on regional, national and international scale is gaining a kind of momentum in the public reception. Rooting in the slow-food and slow-gardening ideology its self-perception is on ecologic soundness, beauty and quality and deliberate and sensual perception of flowers. It is under way to initiate and support local, seasonal, and consciously farmed flowers and foliage. Academics generally have not given too much attention to this phenomenon. In the frame of this research [1] on-farm visits, compiling business profiles and an online-questionnaire among slow-flower-growers were conducted to find out on incentives and motivation, nursery structures and crops, corporate philosophy and gender aspects. The focus had been set on characteristics of the Austrian and German slow-flower-movement (features such as type of operation, farm size, cultivated crops, sales formats, and future visions). The “typical” slow-flower-horticulturist produces flowers, cut flowers and florist green in natural (on field) or semi-protected systems on extensive scale and feels as part of a countermovement to conventional flower production. The potential of slow flowers lies in aesthetics, diversity and distinctiveness that it offers. An increasing demand for slow flowers has a positive impact on the further development and future in a probably new domain in floriculture. One major focus will be put on the aspects of sustainability in horticulture – and the potential of “slow flowers” to contribute to this very demand.

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P6: *Pinus pinea* seedlings demonstrated high resilience in a short but severe drought, indicated by their adaptive biochemical responses

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Stone pine (*Pinus pinea*) has a limited genetic diversity and for future afforestation it is vital to know its drought stress response strategy. Biochemical responses to a short, but severe drought (-4.5 MPa to -4.0 MPa shoot water potential) and to rewatering were tested on seven provenances native to Türkiye with known differences in drought response strategy [1]. Soluble sugars, starch, total non-structural carbohydrates (NSC), proline, malondialdehyde (MDA) and H_2O_2 contents were analyzed in roots, stems, shoots and needles, along with the chlorophyll pigments of needles. All provenances survived water potentials lower than their P_{50} [1], as found for other conifer species [2, 3, 4]. Isohydric species close stomata earlier during drought unless sink activity is downregulated and therefore require more carbohydrate reserves to meet their ongoing carbon demands for respiration, osmoregulation or defense [5]. Isohydric response was associated with high increases of NSC in shoots, soluble sugars in roots, and MDA in needles, shoots and roots as well as an increase in H_2O_2 in needles. Anisohydric response was associated with a significant decrease in needle H_2O_2 and a trend for decreasing carotenoid contents. Increases in starch and NSC in shoots and proline in shoots and roots were significantly lower in the anisohydric group than in the isohydric group. Future research on drought sensitivity of conifers should focus on changes in biochemical traits in several plant organs to see the full picture of drought stress response.

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P7: Ultrastructural analysis of *Clusia* chloroplasts with varying CAM physiotypes

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Clusia is a genus of tropical plants known for their ability to perform Crassulacean Acid Metabolism (CAM), a unique form of photosynthesis that conserves water by opening stomata at night. This adaptation, along with the vital role of chloroplasts in converting stored carbon dioxide into energy during the day, allows *Clusia* plants to thrive in challenging environments. Here, we present a comparative ultrastructural analysis of *Clusia* chloroplasts. Ultrastructural analysis of chloroplasts using transmission electron microscopy (TEM) in different *Clusia species* reveals insights into the potential adaptive mechanisms of Crassulacean Acid Metabolism (CAM) and chloroplast dimorphism. These species, known for their remarkable plasticity in photosynthetic pathways, exhibit distinct leaf anatomies and chloroplast morphologies. TEM highlights variations in thylakoid organization, starch granule accumulation, and plastoglobuli density, reflecting their differential metabolic demands. The study underscores the potential role of chloroplast dimorphism in optimizing photosynthetic efficiency under varying environmental conditions, with mesophyll and bundle sheath chloroplasts displaying structural specialization. This research contributes to understanding the evolutionary and functional significance of CAM and chloroplast dimorphism in Clusia species, offering broader implications for plant adaptation to stress and resource-limited habitats.

P8: Identification of a peculiar chitinase in carnivorous plant species *Drosera binate*

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The genus *Drosera* (sundew) includes over 250 carnivorous plant species. *Drosera binata* thrives in acidic, nutrient-poor soils, using specialized leaves with "flytraps" that secrete hydrolytic enzymes for insect digestion. Among these, chitinases break down the chitin exoskeleton of prey. This study characterizes a specific *D. binata* chitinase involved in prey degradation. The cDNA of chitinase (*DbChitI-3*$^{-S}$) was amplified, cloned into a pET-K2 vector, and expressed in *E. coli* BL21-CodonPlus (DE3) RIL. The recombinant enzyme was purified *via* a Ni-NTA agarose column, and its activity was measured fluorometrically using FITC-chitin as a substrate. Purified DbChitI-3, a class I chitinase with catalytic and chitin-binding domains, exhibited peak activity at pH 2.5–3.0 and temperatures of 15–30°C. It effectively cleaved swollen FITC-chitin and glycol chitin but not shorter substrates. This suggests *DbChitI-3* functions as an endochitinase, without β-N-acetylglucosaminidase or chitobiosidase activity.The acidic nature of digestive fluids in *D. binata* is crucial for prey digestion. The enzyme's activity under highly acidic conditions mirrors chitinases found in animal digestive systems. Additional compounds, such as expansins, may assist in modifying chitin for efficient degradation in plants. Future studies will explore potential biotechnological applications of *DbChitI-3* and its hydrolysis products.

Acknowledgements

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P9: The influence of drought stress on mosses and liverworts

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In their natural habitat, mosses have adapted to repeated drought and wet cycles with poikilohydry, the ability to tolerate desiccation by dormancy and resume the metabolic activity upon rehydration. Aim of this study is to give insights on a morphological, physiological, and cytological level into the response of mosses to dehydration, and rehydration. Five species were selected, *A. undulatum, P. patens, F. hygrometrica, M. polymorpha* were grown in vitro culture, under fixed light, temperature, and humidity parameters, and *P. affine* in the greenhouse. Water loss was measured at in parallel with quantum yield (Φ), a key indicator of photosynthetic activity (48 h), and their correlation determined. One parameter investigated in the rehydration was (Φ) (120 min). Cell, - leaf, - and gametophyte area were evaluated using light microscopy to assess structural changes during dehydration and confocal laser scanning microscopy (CLSM) to determine the cell diameter. A 90 % weight decline after 3-4 hours was seen in all species and remained at this level until 48 hours. (Φ) responses to dehydration showed species-specific decline patterns, with fluctuations. Water weight loss and (Φ) showed strong, positive, correlations (0.90-0.97). Upon rehydration, (Φ) initially increased but then steadily decreased. These results highlight the diverse physiological strategies mosses employ to cope with water loss, offering valuable insights into mechanisms of desiccation tolerance that could inform drought resilience in higher plants.

P10: Cuticle of *Kalmia procumbens* leaves: flavonoids form spines for defence?

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Alpine plant species are exposed to specific abiotic and biotic environmental conditions, such as high altitudes, wind, extreme temperatures and plant-fungus interactions. To cope with such stressors, the alpine azalea *Kalmia procumbens* has developed a thick protective cuticle covering the epidermal cells. By peeling this outermost leaf layer (Fig. 1A) and scanning with a Confocal Raman microscopy through the cuticle we can visualize the change in chemistry from the very top towards the epidermal layer. The bands of the Raman spectra were assigned to cutin, triterpenoids and flavonoids. The latter ones gave the strongest Raman signals and were especially high in the outer part of the cuticle. During the experiment, we noticed that spines formed at the borders of the peel and the surface (Fig. 1B-C). The very intense and sharp Raman spectra of these spines suggest a crystalline nature and the Raman band positions point towards flavonols (Fig. D). In contrast, Kalmia plants having cuticles with no or low flavonoid content did not show such spine formations. Flavonols are reported as response to biotic attacks and when finally, the spines form upon lesions it seems that the chemical defense is supported by mechanical defense.

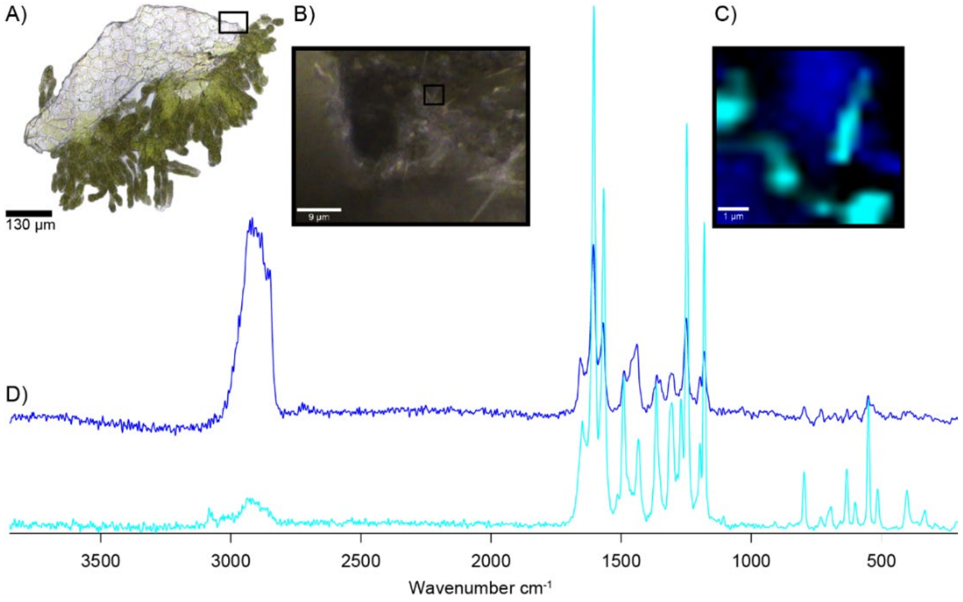

Figure 2: Cuticle peel of *Kalmia procumbens*, A) microscopic overview picture of the upper-side peel, black box indicates caption B), B) sample after one day, formation of spines, black box indicates caption C), C) Raman image based on True Component Analysis (TCA) visualising two chemically different components (blue and cyan) and the D) corresponding average spectra proofing the molecular changes as well as the flavonol nature.

P11: Identification and molecular cloning of a unique protease from carnivorous sundew

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Carnivorous plants grow in nutrient-poor, wet habitats and capture insects by specialized leaves secreting digestive fluid. Decomposition of prey is achieved by a cocktail of hydrolases, including enzymes with proteolytic activity. Hydrolytic enzymes discovered in the trap secretions are a valuable source of proteases for biotechnological applications. The fork-leaved sundew, *Drosera binata*, was aseptically cultivated on supplemented MS medium. Proteins and nucleic acids were extracted from mature trap leaves with glandular tentacles. Preliminary proteomic profiling of induced leaves was conducted by ultrahigh-performance liquid chromatography (Vanquish Neo) coupled to mass spectrometry (Orbitrap Exploris 240). The GenomeWalker (Clontech) DNA walking method was employed to gain the full-length gene sequence of the sundew protease. We generated an enzymatic profile of sundew trap leaves to identify hydrolases underlying digestive processes. From this dataset, we selected a putative cysteine protease that was significantly more abundant in stimulated traps compared to control leaf samples. We then isolated its full-length genomic sequence, which was subjected to comprehensive *in silico* analysis using available bioinformatic tools. Proteomic analysis and subsequent isolation of a protease-coding sequence provided a promising candidate for further recombinant protein expression and its characterization. We identified a unique protease involved in prey digestion that had not been previously described in sundew and isolated its complete gene sequence through molecular cloning.

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P12: Increased pathogen resilience in Pea: Deciphering the Metabolic Code

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Ascochyta blight, caused by *Didymella pinodes*, significantly reduces *Pisum sativum* growth and seed yield. However, not much is known about how some ciltivars contain infection and maintain healthier. Although it has been demonstrated that high levels of Pisatin, an isoflavonoid, sometimes resulted in lower infection of *D. pinodes* [1], our data suggest that Pisatin is not the main metabolite in defense against *D. pinodes*. By monitoring and samplings leaves throughout the infection process, we compare infection scores, primary and secondary metabolite levels, including Pisatin, between cultivar Messire (susceptible) and Protecta (tolerant) over time. The data show that further flavonoids increase substantially especially in the new leaves of the more tolerance cultivar, suggesting further key defense metabolites involved in systemic acquired resilience. This project aims to identify the key flavonoids crucial for enhanced ascochyta resilience.

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P13: *In vitro* Propagation of Ferns

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Ferns, being non-flowering vascular plants, reproduce through spores, making them a valuable model for investigating plant development and adaptation. This research examines the *in vitro* propagation of spores, the development of prothallia, and the preparation of permanent slides to enable detailed microscopic analysis of a fern life cycle. In this study, we investigated the growth rate and development of prothallia in *Nephrolepis* sp. and *Cyrtomium falcatum* from spores cultured on sterile media, in controlled conditions. The samples were regularly checked for the development of archegonia and antheridia, respectively. Subsequently, the samples were fixed and stained with safranin and astrablue. We tested various methods to prepare permanent slides at different stages of the fern life cycle for use in student's courses. Spore sterilisation, germination and prothallium development were successfully observed under controlled conditions, leading to the formation of prothallia with characteristic heart-shaped structures and rhizoids for anchorage. Microscopic analysis of permanent slides revealed well-defined antheridia and archegonia, providing insights into the reproductive structures and developmental stages of the fern gametophyte. Prothallia are short lived structures within a fern's life cycle. Their preservation as permanent slides at different developmental stages is a valuable tool for the microscopic visualization of key structures, highlighting their potential use in research, conservation, and education.

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P14: Crown transparency influences growth dynamics in *Pinus sylvestris* and *Juniperus communis*

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Extended periods of drought and heat have a detrimental effect on the vitality of forests. This decline in vigour is characterised by crown thinning, reduced photosynthesis and declining wood growth rates, as well as increased susceptibility to pathogens. The objective of this study is to conduct an in-situ investigation of the xylem formation dynamics of *Pinus sylvestris* and *Juniperus communis* in relation to their differing crown transparency (ct). The central working hypothesis is that the dynamics of xylem formation are related to the degree of crown transparency. Three vitality classes were selected for each of the two target species (n=20) according to the percentage of crown transparency (ct ≤ 35% low, ct 35-70% medium, ct >70% high). In the course of the 2024 growing season (March to October), microcores (Trephor) of the stem wood were taken at one to three-week intervals, which were cut to 9 µm using a rotary microtome, subjected to vitality staining (Safranin, Astra blue) and quantitatively analysed. The measurements revealed significant differences in growth dynamics and wood increment for both species, depending on the degree of crown transparency. The xylogenetic analysis of microcores confirms the vitality status of woody plants recorded in the field and indicates the influence of the water and/or carbon balance on the intensity and seasonal dynamics of stem growth.

P15: The role of the green cortex in stems from Winter to Spring in *Carpinus betulus* under salt stress

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Salt stress in urban environments is primarily caused by the application of deicing salts during winter, which accumulate in the tree pits of roadside trees. Certain urban tree species, such as *Carpinus betulus*, exhibit high sensitivity to elevated soil NaCl concentrations. Salt uptake through the roots disrupts key physiological processes, including photosynthesis and transpiration, leading to delayed bud break and premature leaf senescence, often as early as late summer. This results in a shortened growing season, reducing the ecological functions of urban trees, such as temperature regulation and air quality improvement. This study investigates the response of *Carpinus betulus*, a widely planted urban tree species in Vienna, Austria, to a salt stress treatment of 5.6 mS NaCl. Preliminary results indicate a pronounced sensitivity to salt exposure, as evidenced by a significant delay in bud break. Additionally, we hypothesize that chlorophyll and carotenoid concentrations in the cortex and xylem, both at the base of the stem and the apical end, fluctuate during the seasonal transition from winter to summer. These pigments are expected to increase until full leaf development and subsequently decline. Moreover, below-ground salt stress may reduce chlorophyll content in stems, thereby interfering with metabolic functions. Understanding these physiological responses is crucial for assessing the long-term impact of salt stress on urban tree health and ecosystem services.

P16: Does H_2S positively influence sulfur metabolism in C_4 plants?

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In C_4 plants, sulfate metabolism is only located in chloroplasts of bundle sheath cells. Glutathione and precursor synthesis is located in mesophyll cells. We assess how sulfur metabolites in maize, a model C_4 plant, respond to sulfur supply via H_2S. Therefore, we detect sulfur metabolites in different subcellular compartments via immunogold-labeling and transmission electron microscopy and quantify the concentrations with software-assisted imaging. Our preliminary data show that subcellular thiol content in maize bundle sheath tissue and mesophyll cells is significantly impacted by H_2S supply. The distribution of sulfur metabolites is compartment specific in both tissues. We propose that non-toxic H_2S treatment may accelerate the flux of glutathione from chloroplasts to the cytosol. This hypothesis is in agreement with the uptake and use of H_2S for the synthesis of thiols and other organic compounds in plants.

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P17: Scytonemin from *Nostoc commune*: A natural compound inducing apoptosis in leukemia cells

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Scytonemin, a bioactive pigment isolated from the cyanobacterium *Nostoc commune*, has been investigated for its antiproliferative and proapoptotic effects on the HL-60 and Jurkat leukemia cell lines [1]. This study aims to analyze the cytotoxic potential of scytonemin and its impact on mitochondrial apoptotic pathways. Cytotoxicity was assessed using the resazurin assay, revealing that SCY exhibited a stronger inhibitory effect on the metabolic activity of leukemia cells (IC50: HL-60 = 60.5 µM, Jurkat = 88.2 µM) compared to the *Nostoc commune* extract [1]. Flow cytometry analysis demonstrated that scytonemin induced G1 phase cell cycle arrest in HL-60 cells, whereas no cell cycle blockade was observed in Jurkat cells [2]. However, a significant accumulation of cells in the subpopulation G0/G1 was detected. Scytonemin significantly increased p21 protein expression and decreased phosphorylated retinoblastoma protein levels in both cell lines. Apoptotic changes were confirmed by phosphatidylserine externalization, loss of mitochondrial membrane potential, cytochrome c release into the cytoplasm, and subsequent activation of caspases 9, 3, and 7. The degradation of PARP protein further confirmed the activation of the mitochondrial apoptotic pathway. Based on these findings, we conclude that scytonemin exerts a strong proapoptotic effect in leukemia cell lines by inducing the mitochondrial apoptotic mechanism. This study highlights the potential of scytonemin as a promising natural compound for future anticancer therapies; however, further *in vivo* studies are necessary to confirm its therapeutic potential.

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P18: Allelopathic effect of lichen secondary metabolites on a photobiont *Asterochloris erici*

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Lichens are symbiotic organisms which consisting of at least two partners. They represent small ecosystem, where interaction within each present microscopic organism is still not well known [1]. Mycobiont produces unique secondary metabolites (SM) which are known as bioactive compounds [2] so far known also as allelochemicals. The photobiont, namely alga *Asterochloris erici* is one of the lichen symbiont, where interaction and response on secondary compounds are not well known [1,3]. In this study we focused on photobiont growth, activity of photosystem II and other parameters which are related to response of photobiont under stress condition. Organic acids of *A. erici* were also analyzed. *A. erici* showed inhibited growth in presence of SM. The chlorophyll *a* expressed as Fv/Fm ratio after exposure decreased. Oxidative stress parameters also showed induction of ROS in treated symbiont. Content of selected organic acids involved in Krebs cycle altered in photobiont cells exposed to the SM. Lichens dispose many unique SM which are of fungal origin. In lichen symbiosis, one of the main representative partners is photobiont (e.g. green algae) and it is in permanent contact with its mycobiont. The phytotoxicity of lichen compounds to algal partners involved in symbiosis were investigated in a few studies so far. We assume that the production of typical SM by mycobiont play key role for maintaining homeostasis in lichen thallus by preventing overgrowth of photobiont biomass in lichen symbiotic organism. Present work highlights photobiont and mycobiont chemical interaction in lichen thalli, phytotoxicity of SM on lichen symbiont is evident, as inferred by documented parameters.

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P19: The lichenization of *Cladonia grayi*: from free-living symbionts to thallus formation

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Lichens are self-sustaining micro-ecosystems formed by the symbiotic interaction of an exhabitant fungus, called “mycobiont”, with extracellular microbial photosynthetic partners, termed “photobiont”, and an indeterminate number of other microscopic organisms. Lichenization, i.e. the transition from the free-living to the symbiotic stage, involves (1) the “pre-contact stage”, (2) the “contact stage”, (3) “envelopment” of algal cells by the fungus, (4) their “incorporation” into a pre-thallus, and (5) “differentiation” into a complex thallus, a unique structure that neither of the symbionts can form alone [1]. We improved *in vitro* culture techniques to induce lichenization under controlled laboratory conditions – a challenge achieved by only a handful of labs globally. Axenic cultures of the lichen *Cladonia grayi* co-cultured on Bold’s Basal Medium with its photobiont *Asterochloris glomerata* atop, were examined using light microscopy and electron microscopy. Hyphal branching and first appressoria formation were observed after three weeks of co-culturing (stage 2). Fungal biomass increased as additional appressoria and haustoria formed, with fungal hyphae beginning to envelop the photobiont (stage 3). An undifferentiated pre-thallus of fungal hyphae and photobiont cells, reminiscent of soredia, formed after several months (stage 4), and experiments are ongoing to reach stage 5. Our next objective is to use this co-culturing approach to trace the exchange of isotopically labelled molecules between symbionts in stages 1 and 2. Controlled lichenisation may enable further studies of photobiont-mycobiont interactions and ultimately determine whether the lichen microbiota is required for lichenization or establishes on a fully formed thallus.

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P20: Underneath agrivoltaics - Physiological study on cherries

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This master's thesis examines the impact of agrivoltaics on their environment, focusing specifically on cherry trees' eco-physiological response to these altered conditions. Electricity generated by photovoltaics is increasing as part of the global energy transition. Furthermore, the implementation of agrivoltaics might open up the possibility of producing crops and electricity within the same area. However, plants underneath agrivoltaics face environmental changes, requiring further investigations on how these altered conditions affect plants' eco-physiological response. Measurements on 32 cherry trees underneath agrivoltaics at research station Haidegg provide SPAD-values, quantum yields, transpiration rates, photosynthetic rates and pigment contents. These are then compared to abiotic data and control groups without agrivoltaics to achieve a complete overview of their eco-physiological response. In general, agrivoltaics create their own microclimate and the trees successfully acclimate to these altered conditions. They accumulate almost every pigment underneath agrivoltaics to enhance light processing, while they show less non-photochemical quenching (NPQ) by zeaxanthin and antheraxanthin. In summary, cherries adjust to agrivoltaics primarily per pigment accumulation.

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P21: A Low-Cost Automated Irrigation System Using Mini-Lysimeters for Improved Drought Stress Experiments with Juvenile Trees

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Controlling water supply is essential for drought stress experiments, but maintaining a stable soil water content manually is challenging and requires constant attention and significant time investment. However, ensuring uniform treatment intensity within a given drought stress level is critical to defining the stress level and reducing variation among plants within a treatment. To address this issue, we adapted the automated irrigation system developed by McCauley & Nackley (2022), which utilizes mini-lysimeters for studies with crops. Our system consists of 32 mini-lysimeters, constructed using load cells (CP 50-3P3, max weight 50 kg, uncertainty: 0.023 %, Kern & Sohn GmbH, Balingen-Frommern, Ger) attached to two aluminum plates, making them suitable for various plant types, including small tree saplings. The load cells are connected to a logger (CR1000, Campbell Scientific Ltd., Logan, UT, USA) that records the weight of each pot and plant every 10 minutes. Based on these measurements, the watering regime can be programmed, for example, to either fully saturate the soil or provide a set percentage of the plant's daily water consumption. Each lysimeter is equipped with an individually controlled magnetic valve (SMC VX21, Tokyo, Jpn), allowing for precise adjustments based on plant size, water consumption, and treatment conditions. The dataset presented here is from a drought stress experiment using saplings of *Ginkgo biloba* (L.), *Fraxinus ornus* (L.), and *Celtis australis* (L.), comparing individual watering regimes and daily water consumption with xylem sap flow (EMS62, EMS, Brno, Cze) and dendrometer (PDS40, EMS, Brno, Cze) data. In order to minimize the effects of wind on the weight measurements, an aluminum grid was constructed to a height of 42 cm around the lysimeters. Depending on the design of the experiment, rainwater input can be prevented by a simple cover of the pot, and soil water loss by a water-tight cover of the pot. Additionally, pot can be equipped with a soil water content and soil temperature sensor (TMS-4, TOMST, Prague, Cze). We believe that automated irrigation systems integrated with lysimeters will reduce variability in drought stress intensity, improving data quality and facilitating analysis. Moreover, our approach is cost-effective, with an estimated cost of 450 € per lysimeter, including the load cell & watering valve.

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P22: Phytomyxids and their interactions with their hosts

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Phytomyxea infect a wide range of hosts, including brown algae and higher plants. Knowledge about phytomyxids is mostly based on the economically important species *Plasmodiophora brassicae*, causing the clubroot disease in Brassicaceae. However, general host-pathogen interaction mechanisms outside the *P. brassiceae* model are poorly understood. By using different fluorescence-based techniques (fluorescence *in situ* hybridization, immunolabelling) in combination with nuclear measurements and the use of publicly available RNA-seq datasets, we reveal basic cellular mechanisms underpinning phytomyxid infections in a non-model pathosystem. We show that infection of the phytomyxid *Maullinia ectocarpii* leads to cell wall changes in its brown algal host. We additionally show that *M. ectocarpii* induces local endoreduplication in its host cells and confirm that *P. brassicae* triggers this process in its plant host as well. This leads to enlarged cells, generating space for the phytomyxids to grow and to produce spores. Additionally, induced endoreduplication likely helps generating a physiological sink in the infected cells, providing the developing parasite with nutrients. We conclude that induced endoreduplication is a conserved mechanism of phytomyxean-host interactions, supported by the discovery of endoreduplication in two phylogenetically distant hosts. Studying elusive phytomyxids helps understanding the biology of this group and spreads light on basic mechanisms of hosts-pathogen interactions.

P23: Potato stress acclimation and signaling under abiotic stress

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Currently heat- drought- and flooding events are increasingly threatening crop production and cause severe losses of harvest. To understand, how plants are able to adapt and acclimate to challenging environmental conditions, it is essential to gain mechanistic insights into these processes. Field trails were done across three years (2021 to 2023) and 5 locations in the Netherlands, Austria, Spain, and Serbia to measure yearly performance of a selection of 44 tetraploid potato cultivars. Additionally, combined heat, drought and waterlogging stress was done in glass house studies applying high-throughput phenotyping and Omics-technologies in two potato varieties with contrasting stress resilience [1,2]. Physiological analysis revealed that regulation of evaporation (indicated by leaf temperature, 2-2B) and a drastic downregulation of photosynthesis (visible by PSII efficiency) were the most striking differences between the two varieties. RNASeq data indicate that at the signaling level Ca^{2+} and SnRK signaling as well as hormone and peptide signaling show strong differences. These data can now be used for modelling of stress response networks [3] und ultimately for development of novel markers for targeted breeding of potato varieties with increased stress resilience.

Acknowledgements

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P24: A single-berry level study on the effect of moderate to severe heat waves on berry cell death in grapevine

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Understanding the consequences of heatwaves on economically important crops such as winegrapes is crucial when considering future climate change scenarios, with increased frequency and intensity of heatwaves. However, studying heat stress and its effects is challenging. Heating heterogeneity within the same cluster (e.g. radiative heating of berries facing direct sunlight as opposed to ones shaded by the canopy) calls for individual monitoring of berries. For this study we used infrared emitters to directly heat the cluster zone of Zweigelt plants grown in a greenhouse chamber. Three heat-stress treatments were imposed: short intense heat for 3 hours, medium heat for 1.5 days, and medium heat for 2.5 days. Thermal imaging was used to monitor the temperature of individual berries and to split them into categories based on the mean temperature reached by the berry (>50 °C, 45-50 °C, etc.). Berries in these categories were sampled after stress and divided in half. One half was used to measure total soluble solids as a measure of ripening stage, while the other half was used to measure electrolyte leakage as a measure of tissue damage from stress. As expected, heat damage was dependent on the temperature reached, although the extent of damage was affected by the ripening stage, with berries in a more advanced ripening stage showing lower damage than unripe ones within the same temperature category. Our results suggest that there are stages during the growing season where heatwaves may pose less of a risk for the yield.

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P25: Impacts of Heavy Metals and Substrate-pH on the Growth of two Moss Species

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Mosses are bioindicators for metal contamination in the environment [1]. However, in natural habitats moss growth is not only impacted by metal contaminations, but also other factors, such as substrate pH and specific metal combinations [2, 3]. This study investigated the effect of differing growth media pH as well as Copper (Cu) and Iron (Fe) contamination on the growth of two moss species (*Physcomitrium patens* and *Pohlia drummondii*). Our experimental setup consisted of *P. patens* and *P. drummondii* that were grown on media containing $CuCl_2$, $FeCl_3$, both metals, and a control group with no metal. All media were prepared at pH 4.8, 5.8, and 6.8. A Nikon SMZ1500 stereomicroscope was used to measure the 2D area of the mosses each week for four weeks to record growth. Both mosses grew most at pH 5.8, except *P. drummondii* with Cu+Fe at pH 6.8, which grew more than any other sample. *P. patens* did not grow on any metal contamination except with Fe at pH 6.8 while *P. drummondii* grew on most contaminations. In line with our results, *P. drummondii* has previously been reported as tolerant to metals, while *P. patens* has not [2, 4]. At the same time, further examination and particularly an increase in sample size is warranted for this study. Overall, our results indicate that metal-toxicity is species-specific, and that substrate pH additionally impacts moss growth. A pH of 5.8 seems best suited for of *P. patens* and *P. drummondii.*

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P26: Iron homeostasis in grapevine rootstocks: Understanding the adaptive mechanisms in response to low iron availability conditions

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Iron (Fe) is an essential element for plant growth and productivity. While Fe is abundant in soil, its availability is often limited [1]. To enhance Fe uptake and utilization, plants have evolved complex strategies to keep cellular Fe homeostasis via several morphological, biochemical, and gene expression changes [2]. This study aimed to identify and differentiate the responsive mechanisms of two grapevine rootstocks under different Fe deficiency conditions. Two grapevine rootstocks, Fercal (tolerant) and 3309C (susceptible), were grown in pots filled with sand for 30 days. The plants were irrigated daily with half-strength Hoagland nutrient solution with modifications according to the applied treatments: i) Control: adequate Fe supply (+Fe), ii) T1: direct Fe deficiency (-Fe), and iii) T2: bicarbonate-induced Fe deficiency (+Fe+BIC). The tolerant rootstock Fercal showed a higher capacity to increase root biomass and maintain stable levels of ferric chelate reductase enzyme activity under both Fe-deficiency conditions. In contrast, 3309C plants experienced a decline in chlorophyll content in their young leaves, leading to more advanced chlorosis symptoms. Additionally, Fercal roots demonstrated an upregulated expression of several genes involved in Fe transport and translocation under both stress conditions. Our findings highlighted distinct response mechanisms developed by each rootstock, which vary depending on the underlying cause of Fe deficiency. Gaining insight into these mechanisms is critical for enhancing Fe efficiency in grapevine rootstocks and promoting sustainable viticulture in adverse soil conditions.

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P27: Chlorophyll a fluorescence as a reliable parameter for photosynthetic activity

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Measuring Chl a fluorescence is a versatile tool in stress physiology [1]. Easy and gentle handling allows consecutive measurements on leaves in vivo. Photosynthetic efficiency (Fv/Fm) and energy conversion (Pi_Abs) are reliable stress markers and can be derived from OJIP measurements, a technique to visualize PSII activity. Methylviologen (MV) is commonly used to induce the production of reactive oxygen species (ROS) increasing oxidative stress [2]. The question was how MV affects fluorescence induction over time (30 minutes to 6 hours). In five independent experiments *A. thaliana* plants were sprayed with 50 µM MV. Treated plants (n=6) were compared to plants sprayed with mock solution (n=6) and to plants without treatment (n=6). OJIP measurements were performed on dark adapted leaves (FluorPen FP 100 – Photo Systems Instruments) and started 30 minutes after spraying with last measurements 6 h after spraying. All experiments showed consistent results, in terms of the differences between the groups and the time courses. Mock treated and untreated plants did not differ significantly. MV-treated plants showed recognizable changes in fluorescence induction in the first measurements after 30 minutes, which increased significantly up to 6 hours. In addition to other paramertes, Fv/Fm and Pi_Abs in particular decreased. Exposure to MV significantly affects *A. thaliana* leaves due to increased ROS production. OJIP measurements allow the evaluation of photosynthetic efficiency in high temporal resolution on intact leaves, providing valuable results for stress experiments. Chl a fluorescence is a versatile component for investigating photosynthetic activity in stress experiments.

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P28: Exploring the role of endophytes for improving cryopreservation of potato

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The potato ranks as the fourth most important food crop. Thus, it is essential to maintain the heterozygous genotypes in vitro to preserve its genetic diversity. In vitro culturing includes surface sterilization to remove external bacteria and fungi, followed by propagation under sterile, sugar-rich conditions. However, this approach is labor-intensive as the plants require periodic transfer to fresh growth medium. Therefore, cryopreservation approaches have been established and implemented in genebanks for long-term storage to preserve vegetatively propagated collections. For this, meristematic tissues, i.e. apical or lateral shoot tips, undergo tissue dissection, osmotic adaptation, cryoprotection, cryogenic treatment using liquid nitrogen to halt all biochemical activity and preserving genetic integrity, and controlled rewarming. However, rewarming can trigger the colonization of endophytes around the explant, which can compromise its ability to develop into a plant/plantlet. In this project, we analyzed 382 potato accessions for their regrowth potential post-cryopreservation. While 50% showed a good regrowth (≥60% of plants regrown), 39% recovered poorly (≤60% of plants regrown) and 11% failed to recover. To investigate microbial influences, an ITS and 16S rRNA gene amplicon survey was conducted on all these accessions. As anticipated, the microbial diversity was in general low due to sterile cultivation conditions. A total of 637 bacterial amplicon sequencing variants (ASVs) spanning 53 different orders were identified. While some ASVs might originate from exogenous sources, others belong to known plant-associated groups, including Bacillales. In addition, bacteria were isolated from 19 potato accessions resulting in 52 bacterial isolates, belonging to 19 different strains based on 16S rRNA gene sequence comparison. The isolates were characterized for their potential in producing IAA, siderophores and osmolytes, as well as in ACC deamination, and phosphate solubilization. This characterization guided the selection of strains isolated from both well and poorly recovering accessions to test their impact on in vitro plant performance and to analyze their genomes. In conclusion, this study provides first insights in the microbial communities associated with potato cryopreservation and their functional traits, representing a crucial step towards enhancing regrowth success and refining long-term preservation strategies in genebanks.

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P29: Towards a new categorization of the anatomical structure of lenticels

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Bark is among the least studied components of a tree, in particular the outer bark, i.e. the periderm and rhytidome [1]. This is despite the importance of bark for overall tree function and survival, which has largely been overlooked until a recent revival of interest e.g. [2-4]. Recent research in tree physiology focuses not only on leaf and wood hydraulics but also on empirical estimation of water loss and water uptake via periderm and eventually the lenticels, e.g. [5-6]. Potential regulatory mechanisms in lenticels for bark transpiration and liquid water uptake remain, however, an enigma [4]. In order to understand functional aspects of lenticels, we intend to investigate their design and also the anatomy of the tissues beneath them. Lenticel structure has been so far analyzed only in ~0.1% of the ~73,000 globally existing tree species and - regarding the high variability in bark anatomy [2] – we need to gain greater knowledge on how conserved lenticel types are within monophyletic clades in order to understand their functional aspects. Within the frame of the project "Smart Bark", the anatomical lenticel design of ~200 different tree species will be histologically analyzed and thereafter tested if the categorization of [7] in three lenticel types holds true or if this classification needs fine-tuning according to potential functional aspects. By gaining more knowledge on the structural variability of periderm and lenticels, we expect hints on potential opening and closing mechanisms and on bark porosity for water vapor and liquid water.

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P30: Proteomic analysis of germinating seeds of parasitic weed—branched broomrape (*Phelipanche ramosa*)

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Broomrapes are obligate holoparasitic plants lacking chlorophyll and entirely dependent on their hosts for nutrients. These parasitic weeds pose a significant threat to agriculture in the Mediterranean region, with climate change potentially expanding their invasion area. Host-induced strigolactones play a crucial role in their germination, but the underlying molecular mechanisms are not fully understood.

Branched broomrape (*Phelipanche ramosa*) seeds collected from a tomato field were conditioned at 25 °C in darkness for 14 days. Next, their germination was induced by 30 min and 2 h treatment with 0.2 µM synthetic strigolactone analog, GR24. Proteome was profiled on Acquity M-Class liquid chromatograph coupled to Synapt G2-Si mass spectrometer. Gene expression was quantified via qPCR on a LightCycler 96 using the δδCT method.

We quantified 1,767 proteins and revealed that 243 were differentially abundant. All differentially accumulated proteins were annotated *de novo*. The majority of proteins showed expected changes during conditioning, resembling stratification in non-parasitic plants.

Proteomic analysis provided insights into strigolactone-induced germination and laid a foundation for future functional research into key regulatory pathways.

Our study highlighted the necessity to advance knowledge on strigolactone perception and signaling for sustainable parasitic weed management.

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P31: Soil microbiome dynamics in response to root exudates from wheat and pearl millet

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Plants interact with the soil microbiome in the rhizosphere through root exudates, significantly altering the soil microbial community [1]. Biological nitrification inhibition (BNI) substances identified in root exudates can enhance the nitrogen use efficiency of agricultural crops [2]. Understanding the dynamics between root exudates and soil microbes is crucial for optimizing management in agricultural systems [3]. In this study, we characterized the rhizosphere microbial communities associated with 20 wheat and 32 pearl millet genotypes using 16S rRNA gene sequencing to assess differences in microbial diversity and composition. Additionally, the BNI activity of root exudates is being measured to explore its correlation with the functional soil microbiome, particularly microbial taxa involved in nitrifying and denitrifying. Our preliminary findings suggest that microbial community composition varies across wheat and pearl millet genotypes, likely driven by genotype-dependent differences in root exudates. These variations may influence microbial functions in the rhizosphere, particularly those involved in BNI and nitrogen transformations. This study will provide further insights into the genotype-mediated interactions among root exudates, soil microbiomes, and BNI, potentially contributing to optimized crop breeding strategies and improved nitrogen use efficiency.

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P32: Water relations of Grüner Veltliner vines unaffected by rootstock variability

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Grapevines are grafted onto rootstocks primarily to protect against grapevine phylloxera root infection. However, rootstocks can impact plant adaptability to varying soil, climate, and water conditions. This study examines the effect of rootstock variability in modulating plant water relations in the Austria's most cultivated grape variety, Grüner Veltliner (GV). We used a GV vineyard grafted onto four commercial rootstocks: Fercal, 5BB, 1103P, and SO4. Key parameters, including plant water potential and stomatal conductance, were monitored over two growing seasons (2023 and 2024) under field conditions in Krems, Austria. Overall, no significant differences in the measured variables were observed between rootstocks. Some transient effects and trends were noted in pre-dawn water potential and g_s, with 1103P exhibiting lower Y and higher g_s, though not consistently throughout the study. No effects on yield nor berry composition were observed at harvest. It is commonly assumed that rootstocks classified as drought-tolerant, such as 1103P, would induce increased canopy growth and water consumption when high soil water availability is present. In the case of GV this does not seem to occur. Transient drought periods were neither intense (Y > -1.4 MPa) nor long in duration (< 7 days), and under such conditions GV seems to behave the same regardless of the rootstock. After two consecutive years of extensive field measurements, our results suggest that the variability due to environmental parameters such as temperature and vapor pressure deficit is higher than the rootstock effect on Grüner Veltliner.

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P33: Understanding Concept Drift in Metabolomics: Predictive analysis of *Arabidopsis thaliana* under cold stress conditions

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In recent years, much attention has been paid to the use of predictive models in metabolomics, particularly in understanding plant responses to environmental stressors. This study aims to detect concept of drift in metabolite concentrations and in different ecotypes of *Arabidopsis thaliana* under two temperature conditions. Concept drift is a phenomenon in which the statistical properties of a target variable change over time, leading to a reduction in the accuracy and reliability of prediction models. Our research aims to address this issue by employing various predictive regression models to analyze metabolomics data, thereby identifying potential confounding factors that may influence plant growth predictions. The study showed that plants in northern Sweden are more adaptable to temperature fluctuations than plants in southern areas. This adaptability is reflected in the concentrations of the simple carbohydrate metabolites – fructose, glucose, galactose and maltose – which serve as indicators for detecting cold stress-related concept drift. Furthermore, the study highlights the importance of considering different ecotypes of *A. thaliana*, as they exhibit varying metabolic patterns that can significantly impact the detection of concept drift. Using the Drift Detection Method (DDM) and the Early Drift Detection Method (EDDM), we detected instances of concept drift in our regression models. The results demonstrate that metabolomics data can effectively detect concept in prediction models, enhancing our understanding of plant responses to changing climate conditions. Future research should explore additional metabolites and their roles in different *A. thaliana* ecotypes under cold stress conditions to further improve concept drift detection and refine predictive models in metabolomics. This study contributes to the growing body of knowledge on plant resilience and metabolic responses, paving the way for more accurate predictions in the face of environmental changes.

P34: Exploring seasonal variations in pigment and antioxidant contents, and the effects of recurrent droughts in *Picea abies* and *Larix decidua*

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Mountain forests provide essential ecosystem services but are increasingly threatened by environmental pressures associated with climate change. We tested whether recurring droughts induce distinct metabolic responses in montane conifers, potentially underpinning species-specific resilience or sensitivity to drought. We examined the responses of *Picea abies* (L.) H. Karst and *Larix decidua* (Mill.) to drought at a long-term ecosystem research site at 1960 m a.s.l. in the Kaserstattalm forest, Tyrolean Alps, where trees were subjected to summer droughts using rainout shelters from 2016 to 2023. Needle samples were collected from two trees in each of three drought-exposed plots and three control plots. Changes in pigment and tocopherol concentrations, and in the redox state of the glutathione (GSH) and glutathione disulphide (GSSG) couple, were analysed via HPLC across eleven time points for *P. abies* and eight for *L. decidua*, spanning summer 2023 to summer 2024, the first year post-drought. Both species exhibited pronounced seasonal variations in the analysed metabolites, but no statistically significant differences in GSH, tocopherol or pigment contents between drought-stressed and control trees. Larch needles contained a pigment that accumulated at all measurement times, particularly intensively in June; preliminary mass spectrometric analyses suggest an unusual chlorophyll modification. More detailed spectroscopic investigations are underway to elucidate the structure of this potentially novel pigment. The absence of significant differences between drought-stressed and control trees – despite documented growth decline in drought-stressed individuals reported in other studies – suggests that these trees may have acclimated their metabolism in response to prolonged drought conditions.

P35: Magnesium Deficiency Disrupts Photosynthetic Performance in Welschriesling: Evidence from Dynamic Gas Exchange Modeling

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Magnesium (Mg) deficiency is a major concern in viticulture, particularly for Welschriesling (WR), a prominent grapevine variety in Austria and Central Europe. This is especially problematic in light soils with high rainfall, where Mg is easily leached and results in impaired photosynthesis and sugar accumulation, which ultimately reduces wine quality. Existing WR clones show limited efficiency in Mg uptake efficiency. To explore the physiological basis of this limitation, we used the LI-6800 portable photosynthesis system to assess photosynthetic performance in 20 grapevine clones (10 Mg-efficient (Mg+), and 10 Mg-deficient (Mg−)) over three weeks. We recorded CO_2 and H_2O exchange at different light and CO2 levels. Data were modeled using established photosynthesis response equations and analyzed with the *gasanalyzer* package in R. Time-dependent trends were evaluated using Spearman correlation via the rstatix package. Key parameters included maximum photosynthetic rate (A_{max}), quantum yield (ϕ), light curve curvature (θ), respiration in the light (R_L), carboxylation capacity (V_{cmax}), electron transport rate at high light (J_{high}), and mesophyll conductance (g_m). In Mg+ clones, parameters remained stable over time. In contrast, Mg− clones showed significant decline in A_{max}, J_{high}, R_L, and ϕ ($p < 0.05$). Notably, V_{cmax} and J_{high} exhibited positive correlations over time in Mg+, but negative correlations in Mg− clones ($p < 0.05$). These results indicate that Mg deficiency impairs photosynthesis by disrupting electron transport and the carboxylation capacity of the Rubisco enzyme. Our findings provide physiological evidence for clone-specific responses and support efforts to select Mg-efficient genotypes for sustainable WR cultivation.

P36: Integrative Transcriptomic and Network Analysis Revealed Candidate Genes Underlying Dwarfism in Rye (*Secale cereale* L.)

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Winter rye, valued for its nutritional content and robustness, often suffers from lodging due to its tall stature, which negatively impacts yield consistency. In contrast to extensively studied cereals like wheat and rice, the molecular underpinnings of dwarfism in rye are poorly understood. This research endeavors to elucidate the molecular mechanisms associated with reduced height in rye, employing a combined transcriptomic and weighted gene co-expression network analysis (*WGCNA*) approach using a near-isogenic line (NIL) population. The plant material consisted of five tall and five dwarf samples from the M112 NILs. RNA was extracted from young leaves and sequenced via the Illumina platform. Differential gene expressions were analyzed using *DESeq2*, and a weighted gene co-expression network was constructed using the *WGCNA* package. Hub genes were defined as those with module membership (MM) > 0.9. Functional enrichment was conducted by identifying orthologs in *Oryza sativa*, *Zea mays*, and *Arabidopsis thaliana*, followed by gene ontology analysis using *gprofilR*. Analysis revealed 685 differentially expressed genes (DEGs), with 619 up-regulated and 66 down-regulated. Notably, a large portion of DEGs clustered in turquoise module, except two down-regulated genes. The gene encoding aldehyde oxidase/xanthine dehydrogenase, implicated in auxin and abscisic acid biosynthesis, displayed the highest MM and was identified as a key hub gene. This candidate genes are currently being validated through qPCR and functional assays. Collectively, these findings contribute crucial insights into the molecular regulation of dwarfism in rye, identifying potential molecular markers for targeted breeding strategies aimed at improving plant architecture and enhancing yield stability.

Note: † The authors contributed equally as first authors

P37: Quantifying Gas Exchange Through Periderm and Lenticels: A Multi-Method Analysis in Branches of Varying Ages of Central European Tree Species

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Gas exchange through the bark of woody plants is crucial for limiting water loss to the environment, allowing oxygen to enter for respiration and for supporting bark photosynthesis. While the inner bark contains living tissues, its function is critically dependent on gas diffusion through the outer bark structures – specifically, the periderm and lenticels. These tissues exhibit differing permeabilities, yet isolating their individual contributions to stem gas exchange remains challenging. To better understand the role of bark surface conductance in regulating water vapour and CO_2 exchange in one-, two-, and three-year-old branches of *Celtis australis* L., *Fraxinus ornus* L., and *Ginkgo biloba* L., we investigated three complementary approaches to quantify the diffusion properties of the periderm and lenticels. Using a LI-6800 connected to a custom-built gas-exchange chamber, we first measured water vapour and CO_2 fluxes from intact stems under controlled environmental conditions, comparing values before and after lenticel sealing to separately quantify periderm and lenticel conductance. In a second approach, we employed a custom-built split-chamber diffusion system, enabling independent control and measurement of gas concentrations in each chamber. Permeability of excised periderm samples, affixed between the chambers, was assessed by monitoring changes in CO_2 and water vapour levels. This setup was validated using a reference membrane with known diffusivity for CO_2 and water vapour. Finally, we applied a gravimetric mass loss technique under standardised environmental conditions to estimate periderm conductance to water vapour, based on temporal changes in sample weight. Together, these methods offer a robust framework for disentangling the contributions of the periderm and lenticels to total stem conductance for both water vapour and CO_2. Our findings aim to improve the quantification of bark photosynthesis by resolving external diffusive limitations, allowing more accurate assessments not only of carbon fluxes and water use, but also of the broader gas exchange dynamics in woody stems of *Celtis australis*, *Fraxinus ornus*, and *Ginkgo biloba* – including implications for respiratory oxygen availability and CO_2 diffusion constraints.

P38: Diversity patterns of herbaceous community in environmental gradients of *dehesa* ecosystems

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Iberian *dehesa* represents a highly biodiverse, semi-natural agrosylvopastoral system where trees, livestock, and pasture coalesce, fostering a dynamic equilibrium between productivity and ecological sustainability. However, in recent decades, a manifold of factors contributed to decline in tree vitality, density, and coverage, leading to long-term changes in species assemblages and ecosystem functionality. This study investigates shifts in herbaceous plants diversity as a function of environmental parameters, phytosanitary state of holm oak *(Quercus ilex* L. subsp. *ballota* (Desf.) Samp.), and potential interactions with biotic agents, including *Phytophthora cinnamomi*. Floristic composition, herbaceous alpha diversity and spatial heterogeneity (beta diversity) patterns were assessed across two *dehesa* stands in southern Spain. Understory diversity was evaluated in relation to environmental gradients and sampling orientation at hierarchical scales encompassing regional, plot, tree, and subplot levels. Results underscore the pivotal role of microsite conditions and macroclimatic variables in structuring herbaceous plant community assemblages. On a broader, regional scale, annual precipitation emerges as a principal determinant of herbaceous diversity and biomass, reflecting its fundamental role as a limiting factor in Mediterranean ecosystems. However, site-specific edaphic properties positively correlate with plant growth and species richness. Notably, microsites resulting from combined effects of plot and tree constitute the primary driver of inter-sample compositional dissimilarity, as evidenced by beta diversity patterns. Contrary to initial hypothesis, our results reveal no significant association between tree health and herbaceous biodiversity.

P39: Inter- and Intraspecific Variation in Elemental Concentrations in Alpine Plants

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Alpine ecosystems are highly sensitive to environmental variation, including differences in soil nutrient availability and microclimate. Plant nutrient concentrations are influenced by both species-specific adaptations and soil properties, but the relative contributions of these factors remain unclear. We measured foliar nutrient and heavy metal concentrations in ten alpine plant species across an elevational gradient on Schrankogel, Tirol, and analyzed the influence of site parameters including soil organic carbon (C), soil C:N ratio, pH and mean summer temperature. The identity of the species had the highest effect on elemental concentration for all elements except Fe, reflecting idiosyncratic differences in nutrient uptake mechanisms and/or demand. However, the relative contribution of environment vs. species differed substantially between elements. Soil, temperature and elevation significantly affected the concentration of most, but not all, elements, but different elements were affected in different ways. For instance, across species the concentration of N, P, Al and Fe increased with elevation, while that of C and Mn declined. These findings highlight the complex interplay between biotic and abiotic factors in shaping alpine plant elemental stoichiometry. Climate change-induced alterations in soil properties and temperature regimes may further impact nutrient dynamics and plant community composition. Nutrients affect plant health and growth, and identifying key drivers of foliar nutrient variability contributes to understanding environmental constraints on plants and the potential effect of climate change. The high variation found in alpine plants and soils makes this an interesting and underexplored system to study plant – soil interactions.

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P40: The best way to stain with Calcofluor White, an example in moss cells.

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Bryophytes take up water and nutrients via the whole plant surface, similar to roots of seed plants. In this study, we investigate the cell shape in order to understand the role of the cell wall in potential metal adsorption. The leaflets of *Physcomitrium patens* consists of a monolayer with only 1 cell width, which makes it the perfect model for microscopy analysis. Here, we specifically focus on confocal light scanning microscopy (CLSM) and developed a way to uniformly stain the cell walls of *P. patens* to get a 3D-reconstruction of different leaflet cells. We used the dye Calcofluor White (CW), which binds to 1–3 beta and 1–4 beta polysaccharides of chitin and cellulose present in cell walls. We used a 1% concentration and added 3 times 0.5 µl with intervals of 15 minutes between them. At the end tap water was added (without washing steps in between) and covered with a cover glass. The best results were obtained when more than 1 exposure to CW was performed. Giving an idea that permeation is the key for a good staining. The images taken from the CLSM contained uniform staining of all cells. The harvesting of the leaflets was a technical challenge. The first staining protocols using only 1 exposition to the CW did not uniformly stain the cells of the leaflet. Also, in the frame of this work, we analyse various leaflet cells to compare their shape with metal adsorption data.

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P41: Influence of Anthocyanins on the Photosynthetic Response of Two Basil Varieties Under Drought Stress

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Drought stress is a critical environmental factor that impairs plant growth and photosynthesis. This study investigates *Ocimum basilicum* L. Italiano Classico (green basil) and *Ocimum basilicum* L. Dark Opal (red basil) to understand how anthocyanins influence their response to drought stress. Chlorophyll fluorescence induction (JIP parameters) and pulse amplitude modulated chlorophyll fluorescence (PAM parameters) were used to assess photosynthetic efficiency. Photosynthetic pigments, anthocyanin content and markers of oxidative stress (malondialdehyde and hydrogen peroxide) were determined. Data revealed that under drought stress the PAM and JIP parameters of chlorophyll fluorescence are less influenced by drought stress in red basil than in green basil. Red basil exhibited significantly smaller increase in malondialdehyde and hydrogen peroxide compared to green basil under drought conditions. The elevated anthocyanin levels in red basil suggest their role as antioxidants, potentially mitigating oxidative damage and enhancing drought tolerance. The responses observed between the two varieties provide insights into the mechanisms of adaptation at reduced water content. This study emphasizes the importance of anthocyanins in drought stress tolerance and contributes to the understanding of physiological responses in *Ocimum basilicum* L. varieties under drought stress.

Acknowledgements

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P42: Dynamic Dark Root Chamber (DDrC): A Novel Approach for Non-Invasive Root Phenotyping in Darkness

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Understanding root development requires non-invasive imaging under natural conditions, where roots remain in darkness while the shoot is exposed to light. Current root phenotyping methods frequently expose roots to light, altering their growth and function. The Dynamic Dark Root Chamber (DDrC) provides a novel solution for continuous, high-resolution imaging of root growth in complete darkness using infrared (IR) illumination [1]. The DDrC is an affordable, customizable root imaging system integrating a Raspberry Pi camera module and IR LEDs to enable stress-free root observation. We employed live imaging, time-lapse recording, and automated data analysis to capture root system architecture dynamics. Root elongation, root angle, and growth rate were monitored under various cultivation conditions and from different barley varieties. The DDrC enables real-time, high-throughput root imaging without disturbing root physiology. Compared to traditional methods, it preserves natural root responses, revealing critical insights into root growth under drought, nutrient limitations, and varying soil textures. The system facilitates multi-day tracking of seminal root emergence, lateral root development, and dynamic root hair adaptation. It is particularly useful for studying genotype-dependent root traits. The DDrC represents a major advancement in non-invasive root phenotyping, enabling realistic studies of root system plasticity. This tool is applicable for breeding programs and fundamental research in root biology.

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P43: Proteomic Insights into the Allelopathic Effects of Usnic Acid on *Physcomitrium patens*

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Allelopathy, the biochemical interaction between plants and surrounding organisms such as cryptogams, other vascular plants and microorganisms [1], plays a crucial role in ecosystem dynamics. Lichens, symbiotic organisms composed of fungi and algae and/or cyanobacteria, produce various secondary metabolites such as usnic acid, known for their potent biological activities [2]. Mosses like *Physcomitrium patens* share habitats with lichens [3] and may experience allelopathic effects from these compounds [4]. This study aims to investigate the proteomic response of *P. patens* to usnic acid exposure, shedding light on its adaptation mechanisms. *P. patens* was treated with usnic acid, and growth area were analyzed. Proteome analysis was performed to identify changes in protein expression. Usnic acid exposure inhibited protonemal expansion while promoting gametophore growth. Proteomic analysis revealed significant changes such as proteins involved in photosynthesis, stress response, and defence mechanisms were up-regulated, whereas some of those linked to energy metabolism and protein biosynthesis were down-regulated. These findings highlight the adaptive responses of *P. patens* under biotic (allelopathy) stress and provide a foundation for further research into the molecular mechanisms governing moss resilience in chemically dynamic environments.

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P44: Thirsty roots: How short-term drought shapes maize (*Zea mays* L.) root exudation patterns

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Root exudates are a complex mixture of metabolites released by roots which influence rhizosphere processes. Under drought, plants alter both the composition and quantity of exuded compounds, with varying responses according to drought severity and genotype-specific traits. This study investigated how short-term drought exposure affects the root exudation dynamics of two maize (Zea mays L.) genotypes with contrasting root hair development: the root-hairless mutant *rth3* and its wild-type (WT) sibling B73. Plants were grown under controlled conditions for 22 days, with drought imposed by withholding irrigation for the last 7 days. Soil water content, transpiration, and gas exchange were monitored daily. At harvest, root exudates were collected for quantitative analysis and metabolite fingerprinting by GC-TOF-MS based non-targeted metabolomics. WT plants exhibited greater biomass, leading to more severe drought stress compared to *rth3*. Transpiration and assimilation rates were initially similar across treatments but began to decline after three days of drought. Drought significantly altered both carbon and nitrogen exudation rates in WT plants, whereas *rth3* exudation rates remained largely unchanged. Both genotypes exhibited shifts in exudate composition, with WT plants increasing osmolyte exudation, particularly sugars and amino acids. This study provides insights into the response of maize to short-term drought stress and highlights the potential contribution of specific metabolites in drought adaptation. These findings contribute to a better understanding of the metabolic strategies used by plants to cope with water limitation and their impact on soil-plant interactions.

P45: Seasonal variations in metabolite and transcript profiles in the streptophyte green alga *Zygogonium ericetorum*

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Some green algae have colonized alpine habitats, in which they have to face high environmental variations within short time periods. Here, the green alga *Zygogonium ericetorum* was examined in its natural alpine environment. The central hypothesis is, that significant changes in primary metabolites and transcriptomic shifts occur due to fluctuations in abiotic factors. This will provide insights into the species acclimation. Field samples were collected monthly from Mount Schönwieskopf (2350 m a.s.l.), Obergurgl, Tyrol, Austria. *In situ*, algae experienced abiotic stress, including high light (~2000 µmol photons m^{-2} s^{-1}), UV-A (~5.5 mW cm^{-2}), UV-B (~23.5 µW cm^{-2}), acidic pH (5.5–6.2), and elevated water temperatures (up to 27.6 °C). To assess stress response, metabolite profiling was conducted via GC-MS, and pigment analysis via HPLC. Differential gene expression analysis using RNA-Seq was performed exemplarily. Metabolite profiling revealed significant seasonal shifts as indicated by principal component analysis (PCA). Non-metric multi-dimensional scaling (NMDS) plot showed UV-A, UV-B and water temperature as significant abiotic factors. Pigment accumulation correlated with metabolic changes, indicating physiological stress responses. August showed the most differential pattern. Preliminary transcriptomic analysis generated 23 million quality-filtered reads, assembled into 108,908 transcripts. Transcriptomic data suggest the presence of *Z. ericetorum* alongside other organisms such as *Scytonema* sp. Our findings enhance our understanding of *Z. ericetorum* acclimation to their natural environment, contributing to broader knowledge on the response to seasonal variations in a stable natural population.

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P46: Root trait adaptation under drought for resilient cropping systems: Insights from two faba bean genotypes grown in different soils

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Grain legumes, such as faba beans (Vicia faba), are core crops contributing to global food security and are becoming increasingly significant amid the growing global shift toward plant-based protein sources. Drought stress significantly threatens legume productivity, adversely affecting yield, nutrient content, and overall agricultural sustainability. While root morphology is recognized for its role in drought adaptation, the influence of root exudation, a key trait shaping plant-soil interactions remains less understood, particularly across different soil environments and plant genotypes. This study investigated drought-induced changes in root traits and exudate composition in two faba bean genotypes (Zoran and Lynx) grown in transparent acrylic columns filled with three soils from distinct agroclimatic zones: Bullionfield (UK), Arvalis (France), and Ptuj (Slovenia). Plants were grown under both optimal and limited water conditions for 21 days. Before harvest, root exudates were collected using the soil-hydroponic-hybrid approach. Biomass, shoot nutrient concentrations, root morphology (WinRhizo), as well as key root exudate compound classes were determined, including total carbon and nitrogen, sugars, amino acids, and phenolic compounds. Our findings show a significant reduction in shoot biomass under drought across all soil types and genotypes, while root biomass exhibited a smaller, soil-dependent decline. Drought significantly increased total carbon (C) exudation rates in both genotypes, along with higher levels of amino acids, phenolic compounds, and soluble carbohydrates. Multivariate analyses (PERMANOVA, PCA) revealed that drought is the most significant factor driving variation in root exudate composition, followed by soil type and plant genotype. Our results suggest a possible adaptive shift in drought-stressed plants towards increased root exudation, potentially as a stress-mitigation strategy, whereas optimal conditions favoured biomass growth. These findings highlight the complex interplay between drought stress, soil environment, and plant genotype in shaping root exudation patterns, emphasizing the need to further explore their role in legume resilience and agricultural sustainability.

P47: Effect of humic acid on photosynthetic activity of green basil under drought stress

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Humic acid, a natural organic compound, has been reported to enhance plant resilience under water-deficit conditions by improving nutrient uptake. The impact of different concentrations of humic acid (1, 3 and 5 mg/ml) under drought stress (20% PEG 6000) on the photosynthetic performance were assessed by chlorophyll fluorescence measurements (PAM and JIP test). The contents of photosynthetic pigment, anthocyanins, phenols, flavonoids as well as the relative water content (RWC), electrolyte leakage, malondialdehyde (MDA) and hydrogen peroxide levels were also measured. The results showed that plants treated with humic acid under drought stress exhibited a better photosynthetic efficiency. The effect was better in plants treated with 5 mg/ml compared to those treated with lower concentrations of humic acid (1 and 3 mg/ml). The findings suggest that humic acid plays a key role in alleviating the adverse effects of drought stress by enhancing antioxidant defense mechanisms, in which phenolic pigments and carotenoids play a crucial role. The important role for the stabilization of photosynthetic activity is also due to increased cyclic electron transport around PSI. The study provides new insights into the beneficial effects of humic acid on basil plants subjected to drought stress, which could be apply for improving plant resilience in water-limited conditions.

Acknowledgements

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P48: Galactose toxicity in plants – a paradox

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Plant cells are surrounded by a carbohydrate-based cell wall, which is continuously remodelled, a process that release sugar monomers. Plants have established recycling pathways to reuse the activated sugars for future polymer biosynthesis. The first step is a phosphorylation of the sugars at the C1-position followed by a conversion to UDP-sugars by a UDP-sugar-pyrophosphorylase, which accepts many different sugar-1-phosphates. This recycling pathway must be tightly controlled as low concentrations (1-3 mM) of external arabinose or galactose cause severe alterations of the root development. Phenotypes include a programmed cell death, defects in cell plate formation after mitosis [1], or increased amounts of glycoproteins. In addition, we observe metabolic changes [2] which likely explain some of the mentioned phenotypes.

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P49: Genetic monitoring of an endangered plant species: the impact of population size, sex ratio, and environmental factors on the genetic diversity of Antennaria dioica

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Understanding the genetic and ecological factors influencing population decline is essential for the conservation of threatened species. Antennaria dioica has experienced a significant population decline in central Germany, making it an important model for studying genetic diversity and ecological interactions in threatened plant species. This study investigates how population size, sex ratio, and environmental conditions influence the genetic diversity of populations and examines historical changes using herbarium data spanning up to 200 years. During field surveys in 2010 and 2022/2023, population size, sex ratio, seedling percentage, vegetation height, percentage of bare soil, and soil depth were recorded. We analysed genetic diversity and population structure using ddRAD sequencing on contemporary (2010 and 2022/2023) and historical herbarium samples. Genetic diversity was positively associated with population size and showed a unimodal relationship with sex ratio, with the highest genetic diversity found in female-biased populations. Herbarium data indicated increased male dominance under drought conditions and a shift to later flowering. These findings highlight the importance of population size and sex ratio in maintaining genetic diversity in A. dioica. The observed shifts in sex ratio and phenology under changing environmental conditions raise concerns about the potential impact of climate change on the species' long-term viability.

P50: Synchrotron source X-ray experiments reveal element specific distributions of heavy metals in moss leaves

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The cell wall of bryophytes is a natural barrier to the environment. It shows a high absorption capacity for water, nutrients, but also heavy metals and therefore bryophytes are often used as biomonitors [1]. The moss *Physcomitrium patens* (Figure 1) is a commonly used model organism for non-vascular plants and is less resistant to heavy metals compared to our second species studied; *Pohlia drummondii*. It has been observed that different metals present in the growth agar have different deleterious effects on these mosses [3]. The samples analyzed were grown in a laboratory environment under stable conditions prior to analysis, allowing precise control of the metals applied. In the talk and the corresponding poster, we will present our approach to quantifying micro-synchrotron X-ray fluorescence data (μ-SRXRF) measured at the PETRA III P06 beamline at DESY in Hamburg, Germany. We will also discuss first results from small-angle X-ray scattering (SAXS) experiments performed at the NanoMAX beamline at MAXIV in Lund, Sweden. The precise special elemental resolution shown in Figure 2 in the nano- to micrometer range can provide new insights into toxicological mechanisms and metal transport in non-vascular plants.

Figure 1: Habitus of *P. patens (*Gametophore), bar=1 cm [4].

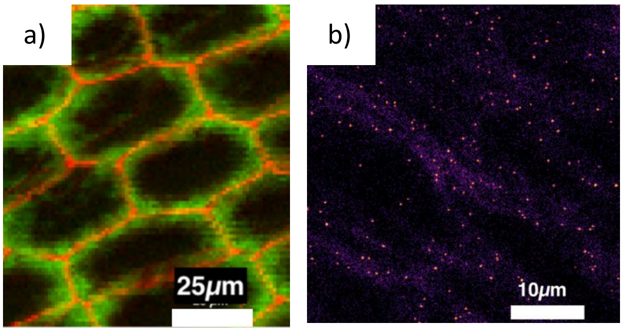

Figure 2: Distribution of Mn (red) and Cl (green) within a leaf of *P. patens*. The high spatial resolution shows Mn is exclusively stored in the cell walls; Cl (green) is also present in the inner cellular space (a). Fe fluorescence signal indicating iron clusters in a leaf of *P. drummondii* sample (b).

References

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